CHAPTER 1

INTRODUCTION

1.1 Historical background

The health insurance is a social intervention that sought to replace the "cash and carry system" of health care financing and to increase access to basic quality health care through the establishment of district-wide insurance schemes in Ghana (International Labour Organization, 2005).

According to Act 650 (2003) of the national health insurance law, the National Health Insurance Authority (NHIA) is authorized to establish the following schemes: District Mutual Health Insurance Scheme, Private Commercial Health Insurance Schemes, and Private Mutual Health Insurance Scheme. Currently, there are 145 district-wide health insurance schemes operating in Ghana of which Brong Ahafo region has 19 administrative centres of NHIS.

According to Act 650 (2003), the role of the National Health Insurance Authority (NHIA) is to register, license, and regulate health insurance schemes and to accredit and monitor health care providers operating under the schemes. It plays a key role in guiding implementation efforts and management of the national health insurance fund.

In order to mobilize funds to support implementation of the district and municipal mutual health insurance schemes, the government of Ghana instituted a health Levy of 2.5 percent on specific goods and services made in or imported to Ghana. In addition, 2.5 percent of the 17.5 percent social security (known as SSNIT) contributions paid by formal sector employees are automatically diverted to support the NHIS. Accordingly, formal sector employees, their dependents, and SSNIT pensioners are automatically enrolled in their district scheme and are exempted from premiums. Additionally, grants and any other voluntary contribution made to the Fund (Act 650, 2003).

1.2 Background of the study

The National Health Insurance Authority (NHIA) is located in Accra. They have regional offices considered as an extension of the operational division of NHIA and are to monitor and evaluate the performance of the administrative centres of NHIS in each region. Brong Ahafo region has nineteen (19) administrative centres of NHIS to monitor and evaluate, and report on performance of each scheme to the head office in Accra.

Despite the fact that electronic means of communication exist among schemes and the regional office in sunyani, an optimal vehicular movement for inspection tour is a problem for the regional authority.

1.3 Statement of the problem

The regional office of NHIA is faced with a problem of how to carry out a physical inspection tour of district schemes known as administrative centres of NHIS to obtain information about their operational challenges particularly in the entry of health claims unto the nationwide information and communication technology platform of NHIA. Lack of inspection and supervision at these administrative centres to ensure that there was limited number of backlog of claims has necessitated the regional authority to carry out this physical inspection tour of district schemes.

The monitoring and evaluation officers were tasked to embark upon an inspection tour of the administrative centres to check on this operational difficulty and report to the regional manager. They were required to maintain a desirable level of movement so as to minimize vehicular fuel consumption.

In this research, we attempt to minimize the vehicular fuel consumption which will reduce cost of travel by finding the optimum distance. The preferred route is illustrated below:

Sunyani Municipal (Initial scheme) →Techiman Municipal → Nkoranza District→ Atebubu→ Sene scheme→ Pru scheme→ Kintampo North → Tano South → Wenchi District→ Jaman South→ Tain District→ Jaman South→ Berekum Municipal → Dormaa District→ Asutifi district →Asunafo South →Asunafo North →Kintampo South →Tano North → Sunyani Municipal.

This preferred route for the inspection tour is without any mathematical model. The study aims at using a mathematical model to determine whether the preferred route is optimum or not.

1.4 Objective of the study

- To model the tour of the Brong Ahafo NHIS administrative centres as Traveling Salesman Problem,
- To determine the optimal distance using the Omicron Genetic Algorithm.

1.5 Significance of the study

The timely inspection tour to district schemes will address concerns on backlog of claims and relatively increase the number of claims entered unto the nationwide information and communication technology platform of NHIA. When this is achieved it becomes easy for the operations division of NHIA to quickly know the amount to be paid to each health service provider by the end of each month. This will ensure that NHIA pay genuine health claims to health service providers and reduce fraud in payment of claims. Economically, the nation will save enough money to improve upon the quality of health delivery in the country and minimize the rate of maternal and child mortality in the country. It will serve as a point of reference for health researchers about diseases that were recorded and treated under the health insurance system in the country.

This study will create the optimal inspection tour road map for the regional authority and contribute to the reduction in atmospheric pollution. This will reduce the rate at which humans inhale toxic wastes from the vehicle and depletion of the ozone layer.

1.6 Methodology and source of data

The inspection tour will be modeled as Traveling Salesman Problem (TSP). Omicron Genetic Algorithm (OGA) will be applied to solve the TSP model to achieve the objective of the research.

The sunyani Roads and Highways Authority will be contacted for the data on physical road networks linking the district where scheme offices are located. Resources available on the internet and the library will be used to obtain the needed literature for this research.

After the relevant data on road distance is obtained, a program code will be written in MATLAB to solve the propose problem. The minimum system requirement for this program to run is Microsoft window XP, with 1 GHz processing speed and hard disk capacity of 20 gigabyte.

1.7 Organization of the study

The thesis is organized into five chapters.

Chapter 1 consists the historical background of the study, the statement of the problem, the objective of the study, significance of the study, methodology and source of data, and organization of the study

Chapter 2 consists the literature review

Chapter 3 covers the methodology which consists of models and methods of solution

Chapter 4 covers the collection of data, analysis and discussion

Chapter 5 consists the conclusion and recommendation

CHAPTER 2

LITERATURE REVIEW

2.1 INTRODUCTION

This chapter presents a brief overview of publications and related works on the application of Traveling Salesman Problem (TSP) to problems facing industries. The traveling salesman problem finds application in a variety of situations such as location-routing problem, material flow system design, post- box collection and vehicle routing.

The traveling salesman first gained fame in a book written by German salesman Voigt in 1832 on how to be a successful traveling salesman. He mentioned the TSP, although not by that name, by suggesting that to cover as many locations as possible without visiting any location twice is the most important aspect of the scheduling of a tour.

According to Applegate et al. (2007), the origin of the name "traveling salesman problem" is a bit of a mystery. This suggests that there is no written documentation pointing to the originator of the name "traveling salesman problem".

Sur-Kolay et al. (2003) defined TSP as a permutation problem with the objective of finding the shortest path (or the minimum cost) on an undirected graph that represents cities to be visited. The TSP starts at one city, visits all other cities successively only once and finally returns to the starting city. That is, given *n* cities and their permutations, the objective is to choose p*i* such that the sum of all Euclidean distances between each city and its successor is minimized. This Euclidean distance between any two cities with coordinate (x1, y1) and (x2, y2) is calculated by, $d = \sqrt{(|x1 - x2|)^2 + (|y1 - y2|)^2}$

The TSP is a classic problem in optimization which has attracted much attention of researchers and mathematicians for several reasons. First, a large number of real-world problems can be modeled through TSP. Secondly, it was proved to be NP-Complete (non-deterministic polynomial-time) problem (Papadimitriou et al., 1997). Thirdly, NP-Complete problems are intractable in the sense that no one has found any really efficient way of solving them for large problem size.

The TSP is known to be NP-hard (Garey and Johnson, 1979). That is, when the problem size is large it takes exponential time to compute and obtain an optimal solution. Over the past decade, the largest TSP was solved involving 7,397 cities (Applegate et al., 1994) and this took 3 to 4 years of computational time. To address this, approximation algorithms or heuristics and metaheuristics (Glover, 1986) have been developed to reduce the computational time.

Karp and Held (1971) improved upon an initial 49 cities TSP solved through the cutting-plane method by Dantzig et al. (1954) and they set a vital precedence by not only solving two larger TSP involving 57-city and 64-city instances but also resolving the Dantzig et al. (1954) 49-city instances.

Crowder and Padberg (1980) presented a remarkable solution that solved 318-city problems. The 318-city instance remained as an impressive solution until further development in 1987 where Padberg and Rinaldi (1987) solved 532-city problems. Grotschel and Holland (1991) extended Dantzig et al. (1954) ideas which gave solutions to 666-city instances.

Applegate et al. (1990) developed computer program called Concorde, written in C programming language, which has been used to solve many instances of TSP. Gerhard Reinelt (1994) published the Traveling Salesman Problem Library (TSPLIB), a collection of benchmark instances of varying difficulty, which had been used by many research groups for

comparing results from instances of TSP. Cook et al. (2005) computed an optimal tour through a 33,810-city instance and 85,900-city instance given by a microchip layout problem, currently the largest solved TSPLIB instance. For many other instances with millions of cities, solutions can be found that are guaranteed to be within 1% of an optimal tour.

The Table 2.0 below indicates the year, the computer program used to obtain solutions for TSP instances and the number of cities that were solved with the Concorde computer program.

Table 2.0 TSP instances and number of cities

Year	Computer program	Number of cities	
1992	Concorde	3038 cities	pcb3038
1993	Concorde	4,461 cities	fnl4461
1994	Concorde	7,397 cities	pla7397
1998	Concorde	13,509 cities	usa13509
2001	Concorde	15,112 cities	d15112
2004	Concorde	24,978 cities	sw24978
2004	Concorde with Domino-Parity	33,810 cities	pla33810
2006	Concorde with Domino-Parity	85,900 cities	pla85900

Since the original aim of TSP formulation is to find the cheapest and shortest tour, it could be applied in transportation processes, logistics, manufacturing, telecommunication, genetics, and neuroscience. A classical TSP application is automatic drilling of printed circuit boards and threading of cells in a testable VLSI (Very Large Scale Integration) circuit (Ravikumar, 1992), and x-ray crystallography (Bland and Shallcross, 1989).

There are many different variations of the traveling salesman problem. First we have the bottleneck traveling salesman problem (Reinelt, 1994) is where we want to minimize the largest edge cost in the tour instead of the total cost. That is, we want to minimize the maximum distance the salesman travels between any two adjacent cities.

The time dependent traveling salesman problem (Lawler et. al., 1986) is the same as the standard traveling salesman problem except we now have time periods. The cost c_{ijt} is the cost of traveling from node *i* to node *j* in time period *t*.

CHAPTER 3

METHODOLOGY

3.1 INTRODUCTION

This chapter presents the models and methods of solution to the Traveling Salesman Problem through Omicron Genetic Algorithm (OGA). We will consider other methods such as tabu search, simulated annealing, genetic algorithm and omicron genetic algorithm that can be applied to solve TSPs. Some work examples would be solved.

3.2 Formulation of the TSP model

The initial approach to solving a TSP is to formulate a mathematical model of the problem. The nature of the formulation looks at administrative centres of NHIS on a map as nodes and draws a line to link each node. These lines are the arc toured by the salesman. The length of a tour is computed as the sum of lengths of the arcs.

The problem is defined as follows;

Let:

i. The total number of nodes on the map is represented as *n*.

ii. The length between each node *i* and node *j* is represented as *d(i, j)*.

iii. For each link x*(i, j)* is 1, if link x*(i, j)* is part of the tour else is 0.

iv. The edges v*(i,j)* = 0, indicates no distance between same node.

v. The set of arcs of the graph is A.

Model for the problem P is:

$$P: \text{MINIMIZE} \quad = \sum_{i,j}^{n} d_{(i,j)} x_{(i,j)} \qquad \textit{equation} \quad (1)$$

Subject to:

$$\sum_{i=1}^{n} x_{(i,j)} = 1 \qquad for \quad all \quad j = 1,2,..,n \qquad equation \quad (2)$$

$$\sum_{j=1}^{n} x_{(i,j)} = 1 \qquad for \quad all \quad i = 1,2,..,n \qquad equation \quad (3)$$

$$\sum_{i,j \in A} x_{(i,j)} \leq (n-1) \quad for \quad all \quad (i,j) \in A, \qquad equation(4)$$

$$x(i,j) \in \{0,1\} \qquad for \quad all \quad i,j = 1,2,..,n \qquad equation \quad (5)$$

Equation (1) is the objective function which will minimize the total length.

Equation (2) ensures that each node is visited from only one other node.

Equation (3) ensures that each node departs to only one other node.

Equation (4) ensures that each tour has not more that n-1 arcs in the set of n.

Equation (5) is the integrality constraint which ensures that the decision variable *x* is either 0 or 1.

In solving the TSP model, factors such as the condition of some roads in the region will not be considered.

3.3 TABU SEARCH (TS)

The Tabu Search is a heuristic method proposed by Glover (1986) to various combinatorial problems. It is one of the best methods used at finding solutions close to optimality in large combinatorial problems encountered in many practical settings.

The principle of TS is to find Local Search whenever it encounters a local optimum by allowing non-improving moves such that cycling back to previously visited solutions is

prevented by the use of memories, called Tabu Lists also referred as Tabu moves (Hillier and Lieberman, 2005), that records the recent history of the search, and this is a key idea that can be linked to Artificial Intelligence concepts.

Pham and Karaboga (2000) outlined three main approaches when performing TS. These are as following: Forbidding approach this strategy control what must be allowed to enter the Tabu list, Freeing approach this strategy determines what exits in the Tabu list and when it exists, and Short-term approach this strategy manages the interplay between the forbidding strategy and freeing strategy to select trial solutions that exist in the tabu list.

Tabu (taboo) search has two basic elements that define its search heuristics, that is, search space and its neighborhood structure. The search space of a TS heuristic is simply the space of all possible solutions that can be considered (visited) during the search. A close link with the definition of search space is the neighborhood structure. Each iteration that is performed on the TSP, the local transformation that can be applied to the current solution, defines a set of neighboring solutions in the search spaces. This search space can be defined as;

N(S) = {solutions obtained by applying a single local transformation to S}

Where *S* denotes current solution and *N(S)* denotes the neighborhood of *S*.

The tabu search algorithm can be summarized into the following steps:

Step 1: Choose an initial solution, i in S. Set $i^* = i$ and $k=0$.

Step 2: Set $k=k+1$ and generate a subset G^* of solution in $N(i, k)$ such that either one of the Tabu conditions is violated or at least one of the aspiration conditions holds.

Step 3: Choose a best j in G^* and set $i=j$.

Step 4: If $f(i) < f(i^*)$ then set $i^* = i$.

Step 5: Update Tabu and aspiration conditions.

Step 6: If a stopping condition is met then stop. Else go to Step 2.

There are some immediate stopping conditions that could be considered. This includes:

1. $N(i, k+1) = 0$. (that is when there are no feasible solution in the neighborhood of solution i)
2. When k is larger than the maximum number of iterations allowed.
3. The number of iterations since the last improvement of i^* is larger than a specified number.
4. When enough evidence can be given that an optimum solution has been obtained.

Hillier and Lieberman (2005) outlined the stopping criterion for Tabu search by, using a fixed number of iterations, a fixed amount of CPU time, or a fixed number of consecutive iterations without an improvement in the best objective function value. Also, stop at any iteration where there are no feasible moves into the local neighborhood of the current trial solution.

Restrictions perform in Tabu search are subject to an important exception. When a taboo (Tabu) move results in a better solution than any previous solution visited, the previous solution is discarded and its Tabu classification may be overridden. A condition that allows such an override to occur is called an aspiration criterion (Glover et al. 1995).

3.3.1Work example

We consider figure 3.0 and apply the Tabu search algorithm to determine the optimal route.

First iteration: *k=0*

Step 1:

Tabu list = [9, 9, 9]

Tabu position= [0, 0, 0, 0, 0, 0, 0, 0, 0]

Tabu state= [0, 0, 0, 0, 0, 0, 0, 0, 3]

Pick at random an initial solution x^0 as order in which the cities were visited.

Thus, x^0= [1, 2, 3, 4, 5, 6, 7, 8, 1]

We compute the objective value as the distance *d(i, j)* between the cities x^0 with reference to equation (1) in section 3.2.

Thus, $d(x^0)$= d(1,2)+ d(2,3)+ d(3,4)+ d(4,5)+ d(5,6)+ d(6,7)+ d(7,8)+ d(8,1) =56

Save x^0 as the best move so far.

Step 2:

The necessary move for x^0 are;

move(2, 3)=[1,3,2,4,5,6,7,8,1]

move(3, 4)=[1,2,4,3,5,6,7,8,1]

move(4, 5)=[1,2,3,5,4,6,7,8,1]

move(5, 6)=[1,2,3,4,6,5,7,8,1]

move(6, 7)=[1,2,3,4,5,7,6,8,1]

move(7, 8)=[1,2,3,4,5,6,8,7,1]

We will apply formula *(i)* to calculate the move value for all the moves *move(i, j)* and choose the best (one with minimum value). Where *i* and *j* represents the move value.

Move*(i, j)*= [d(*i*-1, *j*)+d(*j*, *i*)+d(*i*, *j*+1)] - [d(*i*-1, *i*)+d(*i*, *j*)+d(*j*, *j+1*)] *equation (1)*

Move(2, 3) $i=2$, $j=3$

=[d(2-1, 3)+d(3, 2)+d(2, 3+1)] –[d(2-1, 2)+d(2, 3)+d(3, 3+1)] = 8

Move(3, 4) $i=3$, $j=4$

=[d(3-1,4)+d(4, 3)+d(3, 4+1)] –[d(3-1, 3)+d(3, 4)+d(4, 4+1)] = 1

Move(4, 5) $i=4$, $j=5$

=[d(4-1,5)+d(5, 4)+d(4, 5+1)] –[d(4-1, 4)+d(4, 5)+d(5, 5+1)] = **-7**

Move(5, 6) $i=5$, $j=6$

=[d(5-1,6)+d(6, 5)+d(5, 6+1)] –[d(5-1, 5)+d(5, 6)+d(6, 6+1)] = -4

Move(6, 7) $i=6$, $j=7$

=[d(6-1,7)+d(7, 6)+d(6, 7+1)] –[d(6-1, 6)+d(6, 7)+d(7, 7+1)] = 11

Move(7, 8) $i=7$, $j=8$

=[d(7-1,8)+d(8, 7)+d(7, 8+1)] –[d(7-1, 7)+d(7, 8)+d(8, 8+1)] = 7

since we are looking for minimum solution the best move value is move(4,5)=-7

the new solution is obtained by swapping [4, 5]

Step 3:

The new solution is x^1 = [1, 2, 3, 5, 4, 6, 7, 8, 1]

Objective value x^1 =objective x^0 +move value (4, 5)

= 56 -7

= 49

(i) We do tabu check on the solution x^1 by representing the solution by an attribute of the move operation [4, 5]

Since city 4 is not in the tabu list there is no restriction. We update the Tabu list and its attribute.

Tabu list = [4, 9, 9]

Tabu position = [0, 0, 0, 1, 0, 0, 0, 0, 0]

Tabu state = [0, 0, 0, 1, 0, 0, 0, 0, 2]

(ii) Aspiration check is not necessary since the solution was not Tabu listed

(iii) Check *(i) and (ii)* are successful hence we keep the new solution

x^1 = [1, 2 ,3 , 5, 4, 6, 7, 8, 1] = 49

Step 4

Since objective x^1 < objective x^0, the best solution is 49 with move (4, 5). Assign $x^0 \leftarrow x^1$.

x^1 has the best current solution and has the best move value that it is being Tabu listed.

Step 5

The loop condition is the stated number of iterations that do not bring any improved solution. After such number of iteration we go to step 6 to restart the Tabu search with a new solution.

Step 6

This step may not be necessary since the improved solution has been obtained.

Second iteration: *k=1*

Step 2:

The new solution x^0 = [1, 2, 3, 5, 4, 6, 7, 8, 1]

The necessary move for x^0 are;

move(2, 3)= [1, 3 ,2 , 4, 5, 6, 7, 8, 1]

move(3, 5)= [1, 2 ,5 , 3, 4, 6, 7, 8, 1]

move(5, 4)= [1, 2 ,3 , 4, 5, 6, 7, 8, 1]

move(4, 6)= [1, 2 ,3 , 5, 6, 4, 7, 8, 1]

move(6, 7)= [1, 2 ,3 , 5, 4, 7, 6, 8, 1]

move(7, 8)= [1, 2 ,3 , 5, 4, 6, 8, 7, 1]

we will calculate the move value and choose the best move

Move(2, 3) i=2 , j= 3

=[d(2-1, 3)+d(3, 2)+d(2, 3+1)] –[d(2-1, 2)+d(2, 3)+d(3, 3+1)] = 8

Move(3, 5) *i=3, j= 5*

=[d(3-1,5)+d(5, 3)+d(3, 5+1)] –[d(3-1, 3)+d(3, 5)+d(5, 4+1)] = 7

Move(5, 4) *i=5, j= 4*

=[d(5-1,4)+d(4, 5)+d(5, 4+1)] –[d(5-1, 5)+d(5, 4)+d(4, 4+1)] = -12

Move(4, 6) *i=4, j= 6*

=[d(4-1,6)+d(6, 4)+d(4, 6+1)] –[d(4-1, 4)+d(4, 6)+d(6, 6+1)] = -5

Move(6, 7) *i=6, j= 7*

=[d(6-1,7)+d(7, 6)+d(6, 7+1)] –[d(6-1, 6)+d(6, 7)+d(7, 7+1)] = 11

Move(7, 8) $i=7, j=8$

=[d(7-1,8)+d(8, 7)+d(7, 8+1)] –[d(7-1, 7)+d(7, 8)+d(8, 8+1)] = 7

since we are looking for minimum solution the best move value is move (5,4)=-12

the new solution is obtained by swapping [5, 4]

Step 3:

The new solution is x^1 = [1, 2, 3, 5, 4, 6, 7, 8, 1]

Objective value x^1 =objective x^0 +move value (5, 4)

= 49 -12

= 37

(i) Tabu check shows that city 5 is not in the Tabu list. We update the tabu restrictions.

Tabu list = [5, 4, 9]

Tabu position = [0, 0, 0, 1, 1, 0, 0, 0, 0]

Tabu state = [0, 0, 0, 1, 1, 0, 0, 0, 1]

(ii) Aspiration check is not necessary

(iii) Check *(i) and(ii)* are successful hence we keep the new solution

x^1 = [1, 2, 3, 5, 4, 6, 7, 8, 1]

Step 4:

Since objective x^1 < objective x^0, the best solution is 37 with move (5, 4). Assign $x^0 \leftarrow x^1$.

x^1 has the best current solution and has the best move value that it is being Tabu listed.

Step 5

The loop condition is the stated number of iterations that do not bring any improved solution. After such number of iteration we go to step 6 to restart the Tabu search with a new solution.

Step 6

This step may not be necessary since the improved solution has been obtained.

The Tabu search continues until the optimal solution is obtained.

3.4 SIMULATED ANNEALING (SA)

Simulated Annealing (SA) is a probabilistic metaheuristics method proposed by Kirkpatrick, Gelett and Vecchi (1983) and Cerny (1985) for locating a good approximation to a global optimum of a given cost function in a discrete search space.

Simulated annealing algorithm according to Mahmoud (2007) is a general purpose optimization technique. It has been derived from the concept of metallurgy in which we have to crystallize the liquid to required temperature. In this process the liquids will be initially at high temperature and the molecules are free to move. As the temperature goes down, there shall be restriction in the movement of the molecules and the liquid begins to solidify. If the liquid is cooled slowly enough, then it forms a crystallize structure. This structure will be in minimum energy state. If the liquid is cooled down rapidly then it forms a solid which will not be in minimum energy state. Thus the main idea in simulated annealing is to cool the liquid in a control matter and then to rearrange the molecules if the desired output is not obtained. This rearrangement of molecules will take place based on the objective function which evaluates the energy of the molecules in the corresponding iterative algorithm. SA aims to achieve global optimum by slowly converging to a final solution, making downwards move hoping to reach global optimum solution.

The application of simulated annealing to TSP usually starts with a random generation and performs a series of moves to change the generation gradually. Temperature is gradually decreased from a high value to a value at which it is so small that the system is frozen. For TSP, the energy decreases is given by the difference between the lengths of the current configuration and the new configuration.

The simulated annealing algorithm can be summarized into the following steps:

Step 1: Generate a starting solution x and set the initial solution as $x^{(0)} = x$.

Step 2: set an initial counter as k=0, and determine an appropriate starting temperature T.

Step 3: as long as the temperature is larger than some set value, do the following

Step 4: choose a new solution $x^{(1)}$ in the neighborhood of $x^{(0)}$

Step 5: compute δ = *distance* (x^1) – *distance* (x^0)

Step 6: if $\delta > 0$, accept the new solution $x^{(1)}$ and assign $x^{(0)} \leftarrow x^{(1)}$ and keep $x^{(0)}$ as the new solution

Step 7: else generate random number θ in (0, 1)

Step 8: if the random number $\theta \leq e^{-\left(\frac{\delta}{T}\right)}$, then set $x^{(0)} \leftarrow x^{(1)}$

Step 9: until iteration counter equals the maximum iteration number goto step 5

Step 9: stop when the temperature is lower or stopping condition

Step 10: when a best solution x is not obtained continue to step 1 and set $k=k+1$, else end.

3.4.1 Work example

A salesman chooses a route to visit each city exactly once starting from city 1 and return to the same city. The number on the edge linking to the next city is the distance between each city. We consider that the reverse distance is the same in each direction. The objective is to determine the route that will minimize the total distance that the salesman should travel.

The figure below shows the network of a traveling salesman problem with eight cities. City 1 is the starting point of the salesman.

Figure 3.0 Traveling Salesman Problem

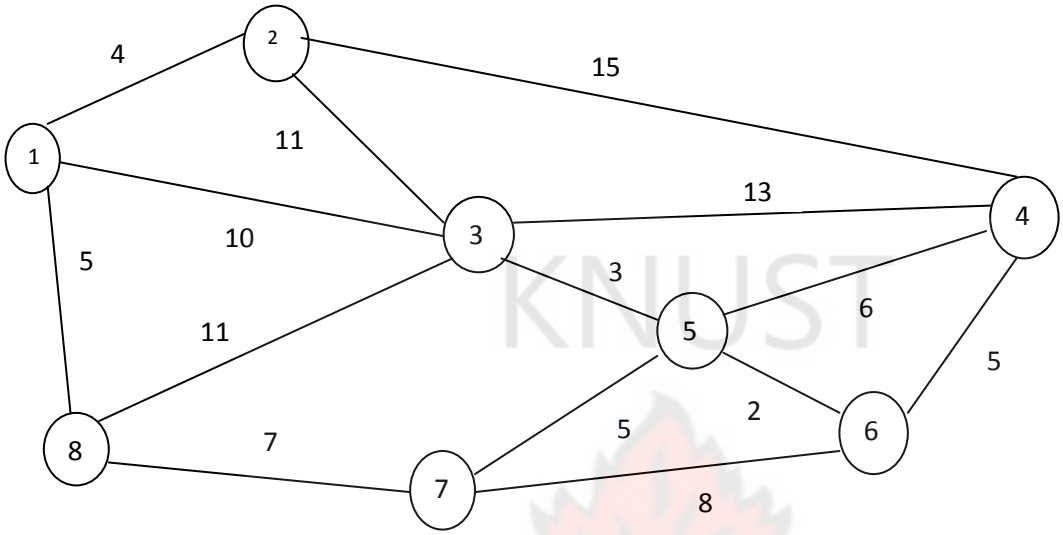


Table 3.0 Distance matrix

Node	1	2	3	4	5	6	7	8
1	0	4	10	19	13	15	12	5
2	4	0	11	15	14	16	16	9
3	10	11	0	9	3	5	8	6
4	19	15	9	0	6	5	11	15
5	13	14	3	6	0	2	5	9
6	15	16	5	5	2	0	7	11
7	12	16	8	11	5	7	0	7
8	5	9	15	18	12	14	7	0

Considering figure 3.0, we will take the initial solution for the tour as;

x=1-2-3-4-5-6-7-8-1

We compute the objective value as the distance $d(i, j)$ between the cities x^0 with reference to equation (1) in section 3.2.

The parameters to use are;

Initial temperature T_0=20,

Updating of temperature (T_k) , $T_{k+1} = \alpha T_k$ and α=0.85

Stopping criteria T < 5 (final temperature)

Starting Iteration: *k*=0

x^0=1-2-3-4-5-6-7-8-1

$d(x^0)$=d(1,2)+ d(2,3)+ d(3,4)+ d(4,5)+ d(5,6)+ d(6,7)+ d(7,8)+ d(8,1)

$d(x^0)$=56

Generate a new solution x^1 in the neighborhood of x^0 such as x^1 =1-3-2-4-5-6-7-8-1

$d(x^1)$=d(1,3)+ d(3,2)+ d(2,4)+ d(4,5)+ d(5,6)+d(6,7)+ d(7,8)+ d(8,1)

$d(x^1)$=64

$\delta = d(x^1) - d(x^0)$

= 64 – 56 = 8

Form minimization problem we expected that $d(x^1)$ will be less than $d(x^0)$ then we would have chosen x^1= 1-3-2-4-5-6-7-8-1 as the new solution.

Since $\delta = 8 > 0$, we would normally discard x^1 as non-improving solution. Simulated annealing procedure requires that we perform further test before discarding x^1.

We would apply the Boltzmann's condition $m = e^{-\left(\frac{\delta}{T}\right)}$, $m = e^{-\left(\frac{8}{20}\right)} = 0.6703$

We would generate random numbers from a computer as $\theta = 0.480$.

Since 0.6703 > 0.480 we do not discard x^1 but set x^1 as new solution such as $x^0 \leftarrow x^1$

Since the stopping criterion (T < 5) is not met

We then update the temperature $T_1 = \alpha T_0 = 0.85(20) = 17$, and set $k = k+1$

Second iteration: *k=1*

$d(x^0) = 64$

we generate a new solution for the tour as 1-2-4-3-5-6-7-8-1

x^1 =1-2-4-3-5-6-7-8-1

$d(x^1)$=d(1,2)+ d(2,4)+ d(4,3)+ d(3,5)+ d(5,6)+d(6,7)+ d(7,8)+ d(8,1)

$d(x^1) = 57$

$\delta = d(x^1) - d(x^0)$

$= 57 - 64 = -7$

Since the computed $\delta < 0$ we then set $x^0 \leftarrow x^1$

Since the stopping criterion (T < 5) is not met

We update the temperature $T_2 = \alpha T_1 = 0.85(17) = 14$, and increase k by 1

Third iteration: *k=2*

$d(x^0) = 57$

we generate a new solution for the tour as 1-2-3-5-4-6-7-8-1

x^1 =1-2-3-5-4-6-7-8-1

$d(x^1)$=d(1,2)+ d(2,3)+ d(3,5)+ d(5,4)+ d(4,6)+d(6,7)+ d(7,8)+ d(8,1)

$d(x^1) = 49$

$\delta = d(x^1) - d(x^0)$

$= 49 - 57 = -8$

Since the computed $\delta < 0$ we then set $x^0 \leftarrow x^1$

Since the stopping criterion ($T < 5$) is not met

We update the temperature $T_3 = \alpha T_2 = 0.85(14) = 11.9$, and increase k by 1

We continue with the iteration until the stopping condition is met.

3.5 ANT COLONY OPTIMIZATION (ACO) TECHNIQUE

Ant colony optimization (Marco Dorigo, 1992) is a technique use for solving computational problems, based on various aspects of the behavior of real ants seeking a shorter path between their colony and a source of food without using visual cues (Hölldobler and Wilson, 1990). Real ants are capable of adapting to changes in the environment, for example finding a new shortest path once the old one is no longer feasible due to a new obstacle (Beckers et al. 1992). Once the obstacle has appeared those ants can find the shortest path that reconnects a broken initial path. Ants which are just in front of the obstacle cannot continue on the path and therefore they have to choose between turning right or left. In this situation we can expect half the ants to choose to turn right and the other half to turn left.

The idea of this algorithm involves movement of ants in a colony through different states of a problem influence by trails and attractiveness. Each ant gradually constructs a solution to a problem, evaluates the solution and modifies the trail values on the components used in its solution. The algorithm has a mechanism to reduce the possibility of getting stuck in local optima (called trail evaporation) and biasing the search process from a non-local perspective

(called daemon actions). Ants exchange information indirectly by depositing pheromones detailing the status of their work which only ants located where near can have a notion of them. The following are some variations of the algorithm:

(i) ***Elitist ant system.*** The global best solution deposits pheromone, detailing the status of their work, on every iteration along with all the other ants.

(ii) ***Max-Min ant system (MMAS).*** Added Maximum and Minimum pheromone amounts $[\tau_{max},\tau_{min}]$ Only global best or iteration best tour deposited pheromone and all edges are initialized to τ_{max} and reinitialized to τ_{max} when nearing stagnation (Hoos and Stützle, 1996).

(iii) ***Rank-based ant system (ASrank).*** This system ranks all solutions according to their fitness. The amount of pheromone deposited is then weighted for each solution, such that the solutions with better fitness deposit more pheromone than the solutions with worse fitness.

(iv) ***Continuous orthogonal ant colony (COAC).*** The pheromone deposit mechanism is to enable ants to search for solutions collaboratively and effectively by using an orthogonal design method, ants in the feasible domain can explore their chosen regions rapidly and efficiently, with enhanced global search capability and accuracy. The orthogonal design method and the adaptive radius adjustment method can also be extended to other optimization algorithms for delivering wider advantages in solving practical problems.

Ant colony optimization algorithms have been applied to many combinatorial optimization problems, ranging from assignment problem to routing vehicles, network routing and urban transportation systems, Scheduling problem, knapsack problem, Connection-oriented network routing (Caro and Dorigo, 1998), Connectionless network routing, Discounted cash flows in project scheduling (Chen et al., 2010), and a lot of derived methods have been adapted to dynamic problems in real variables, stochastic problems, multi-targets and parallel implementations. Ant colony optimization algorithms have been used to produce near-optimal

solutions to the travelling salesman problem. Even though there exist several ACO variants, the one that may be considered a standard approach is presented next.

3.5.1 Standard Approach

ACO uses a pheromone matrix $\tau = \{\tau_{ij}\}$ for the construction of potential good solutions. The initial values of τ are set $\tau_{ij} = \tau_{init}$ $\forall(i, j)$, where $\tau_{init} > 0$. It also takes advantage of heuristic information using $\eta_{ij} = 1/d(i, j)$. Parameter α and β defines the relative influence between the heuristic information and then pheromone levels. While visiting city i, N_i represents the set of cities not yet visited and the probability of choosing a city j at city i is defined by equation *(i);*

$$P_{i,j} = \begin{cases} \frac{{\tau_{i,j}}^{\alpha} * {\eta_{i,j}}^{\beta}}{\sum_{\forall h \in Ni} {\tau_{i,j}}^{\alpha} * {\eta_{i,j}}^{\beta}}, & if\ j \in \mathrm{N}_i \\ 0, & otherwise \end{cases} \quad (i)$$

At every generation of the algorithm, each of the m ants constructs a complete tour using (1), starting at a randomly chosen city. Pheromone evaporation is applied for all (i, j) according to $\tau_{ij} = (1 - \rho) \cdot \tau_{ij}$, where parameter $\rho \in (0, 1]$ determines the evaporation rate. Considering an elitist strategy, the best solution found so far r_{best} updates τ according to $\tau_{ij} = \tau_{ij} + \Delta\tau$, where $\Delta\tau = 1/l(r_{best})$ if $(i, j) \in r_{best}$ and $\Delta\tau = 0$ if $(i, j) /\in r_{best}$. For one of the best performing ACO algorithms, the *MAX-MIN* Ant System (*MMAS).*

3.5.2 Population-based ACO

The Population-based ACOs (P-ACOs) were designed by Guntsch and Middendorf (2006) for dynamic combinatorial optimization problems. As the standard approach, the initial values of τ are set $\tau_{ij} = \tau_{init}$ $\forall(i, j)$, where $\tau_{init} > 0$. The P-ACO approach updates in a different way the pheromone information than the standard approach. P-ACO derives the pheromone matrix through a population $Q = \{Qx\}$ of q good solutions or individuals as follows. First, at every iteration each of the m ants constructs a solution using probabilities given in equation (1), the

best solution enters the population Q. Whenever a solution Qin enters the population, then τij is updated according to $\tau_{ij} = \tau_{ij} + \Delta\tau$, where $\Delta\tau = \Delta$ if $(i, j) \in Q_{in}$ and $\Delta\tau = 0$ if $(i, j) / \in Q_{in}$. After the first q solutions enter Q, i.e. the initialization of the population is finished, one solution Q_{out} must leave the population at every iteration. The solution that must leave the population is decided by an update strategy. Whenever a solution Q_{out} leaves the population, then $\tau_{ij} = \tau_{ij} - \Delta\tau$, where $\Delta\tau = \Delta$ if $(i, j) \in Q_{out}$ and $\Delta\tau = 0$ if $(i, j) / \in Q_{out}$. P-ACO replaces the pheromone evaporation used by the standard approach in this way. The value Δ is a constant determined by the following input parameters, size of the population q, minimum or initial pheromone level $\tau init$ and maximum pheromone level τ_{max}. Thus, $\Delta = (\tau_{max} - \tau_{init})/q$ (Guntsch and Middendorf, 2006).

3.5.2.1 FIFO-Queue Update Strategy

The FIFO-Queue update strategy was the first P-ACO strategy designed by Guntsch and Middendorf (2006), trying to simulate the behavior of the standard approach of ACO. In the FIFO-Queue update strategy, Q_{out} is the oldest individual of Q.

3.5.2.2 Quality Update Strategy

A variety of strategies were studied by Guntsch and Middendorf (2002) and one of them is the Quality update strategy. The worst solution (considering quality) of the set $\{Q, Q_{in}\}$ leaves the population in this strategy. This ensures that the best solutions found so far make up the population.

3.5.3 Omicron ACO

In the search for a new ACO analytical tool, Omicron ACO (OA) was developed by Gómez and Barán (2004). OA was inspired by *MMAS*, an elitist ACO currently considered among the

best performing algorithms for the TSP Stützle and Hoos (2000). It is based on the hypothesis that it is convenient to search nearby good solutions by Stützle and Hoos (2000).

The main difference between *MMAS* and OA is the way the algorithms update the pheromone matrix. In OA, a constant pheromone matrix $\tau 0$ with $\tau 0_{i,j} = 1, \forall_{i,j}$ is defined. OA maintains a population $Q = \{Q_x\}$ of q individuals or solutions, the best unique ones found so far. The best individual of Q at any moment is called $Q*$, while the worst individual Q_{worst}.

In OA the first population is chosen using $\tau 0$. At every iteration a new individual Q_{new} is generated, replacing $Q_{worst} \in Q$, if Q_{new} is better than Q_{worst} and different from any other $Q_x \in Q$. After K iterations, τ is recalculated using the input parameter Omicron (O). First, $\tau = \tau 0$; then, O/q is added to each element τ_{ij} for each time an arc (i, j) appears in any of the q individuals present in Q. The above process is repeated on every k iteration until the end condition is reached. Note that $1 \leq \tau_{ij} \leq (1 + O)$, where $\tau_{ij} = 1$ if arc (i, j) is not present in any Q_x, while $\tau_{ij} = (1 + O)$ if arc (i, j) is in every Q_x.

Even considering their different origins, OA results are similar to the Population-based ACO algorithms described by Guntsch and Martin Middendorf (2002). The main difference between the OA and the *Quality* Strategy of P-ACO is that OA does not allow identical individuals in its population. Also, OA updates τ on every k iterations, while P-ACO updates τ every iteration.

The ACO algorithm can be summarized into the following steps:

Step 1: Generate random individuals from initial population derived from a pheromone matrix

Step 2: initialize an iteration counter k=0

Step 3: update the pheromone matrix

Step 4: generate new individual using the updated pheromone matrix

Step 5: the new individual replaces the worst individual solution in the initial population.

Step 6: increment of the iteration counter k=k+1

Step 7: stop, if the termination condition is met.

3.6 GENETIC ALGORITHM (GA)

GA is a class of evolutionary algorithms inspired by Darwin (1859) a theory of "survival of the fittest" (Herbert Spencer, 1864) and further discussed by Dawkins (1986). Genetic algorithm has the biological principle that species live in a competitive environment and their continuous survival depends on the mechanics of "natural selection" (Darwin, 1868). This algorithm uses a technique such as inheritance, mutation, selection and crossover (also referred as recombination). Holland (1975) invented genetic algorithm as an adaptive search procedure.

GA is also an efficient search method that has been used for path selection in networks. GA is a stochastic search algorithm which is based on the principle of natural selection and recombination. A GA is composed with a set of solutions, which represents the chromosomes. This composed set is referred to as population. Population consists of set of chromosome which is assumed to give solutions. From this population, we randomly choose the first generation from which solutions are obtained. These solutions become a part of the next generation. Within the population, the chromosomes are tested to see whether they give a valid solution. This testing operation is nothing but the fitness functions which are applied on the chromosome. Operations like selection, crossover and mutation are applied on the selected chromosome to obtain the progeny. Again fitness function is applied to these progeny to test for its fitness. Most fit progeny chromosome will be the participants in the next generation. The best sets of solution are obtained using heuristic search techniques.

The performance of GA is based on efficient representation, evaluation of fitness function and other parameters like size of population, rate of crossover, mutation and the strength of

selection. Genetic algorithms are able to find out optimal or near optimal solution depending on the selection function Goldberg and Miller (1995); Ray et. al (2004).

According to Dr. Amponsah and Darkwah (2007), the genetic algorithm introduced by Holland had the following similarity of the evolutionary principles.

Table 3.1 below compares evolution to genetic algorithm.

Evolution	**Genetic Algorithm**
An **individual** is a genotype of the species	An **individual** is a solution of the optimization problem
Chromosomes define the structure of an individual	**Chromosomes** are used to represent the data structure of the solution
Chromosomes consists of sequence of cells called **genes** which contain the structural information	Chromosome consists of a sequence of gene species which are **placeholder boxes** containing string of data whose unique combination give the solution value
The genetic information or trait in each gene is called an **allele**	An **allele** is an element of the data structure stored in a gene placeholder
Fitness of an individual is an interpretation of how the chromosomes have adapted to the competitive environment	**Fitness** of a solution consists in evaluation of measures of the objective function for the solution and comparing it to the evaluations for other solutions
A **population** is a collection of the species found in a given location	A **population** is a set of solutions that form the domain search space.
A **generation** is a given number of individuals of the population indentified over a period of time.	A **generation** is a set of solutions taken from the population (domain) and generated at an instant of time or in an iteration
Selection is pairing of individuals as parents for reproduction	**Selection** is the operation of selecting parents from the generation to produce offspring.

Crossover is mating and breeding of offspring by pairs of parents whereby chromosomes characteristics are exchanged to form new individuals.	**Crossover** is the operation whereby pairs of parents exchange characteristics of their data structure to produce two new individuals as offspring.
Mutation is a random chromosomal process of modification whereby the inherited genes of the offspring from their parents are distorted.	**Mutation** is random operation whereby the allele of a gene in a chromosome of the offspring is changed by a probability pm.
Recombination is a process of nature's survival of the fittest.	**Recombination** is the operation whereby elements of the generation and elements of the offspring form an intermediate generation and less fit chromosomes are taken from the generation.

The two distinct elements in the GA are individuals and populations. An individual is a single solution while the population is the set of individuals currently involved in the search process.

Given a population at time *t*, genetic operators are applied to produce a new population at time *t+1*. A step- wise evolution of the population from time *t* to *t+1* is called a generation. The Genetic Algorithm for a single generation is based on the general GA framework of Selection, Crossover, Mutation and Recombination.

3.6.1 Representation of individuals

A gene is a bit string of arbitrary lengths. The bit string is a binary representation of number of intervals from a lower bound. A gene is the GA's representation of a single factor value for a control factor, where control factor must have an upper bound and lower bound. This range can be divided into the number of intervals that can be expressed by the gene's bit string. A bit string of length 'n' can represent (2^n-1) intervals. The size of the interval would be

(range)/(2^n-1). The structure of each gene is defined in a record of phenotyping parameters. The phenotype parameters are instructions for mapping between genotype and phenotype. It can also be said as encoding a solution set into a chromosome and decoding a chromosome to a solution set. The mapping between genotype and phenotype is necessary to convert solution sets from the model into a form that the GA can work with, and for converting new individuals from the GA into a form that the model can evaluate. In a chromosome, the genes are represented as in Figure 3.1

Figure 3.1 Representation of a gene

1010	1110	1111	0101

gene 1 gene 2 gene 3 gene 4

3.6.2 Fitness function

According to Sivanandam and Deepa (2008), the fitness of an individual in a genetic algorithm is the value of an objective function for its phenotype. For calculating fitness, the chromosome has to be first decoded and the objective function has to be evaluated. The fitness not only indicates how good the solution is, but also corresponds to how close the chromosome is to the optimal one. In TSP formulation the fitness function is the sum of the paths between the cities.

$$f = \sum_{i=1}^{n} d(c_i, c_{(i+1)})$$

$d(,)$ *is a distance function*

n *is number of cities*

c_i *is the ith city.*

3.6.3 Population

A population is a collection of individuals. A population consists of a number of individuals being tested, the phenotype parameters defining the individuals and some information about search space. The two important aspects of population used in Genetic Algorithms are; the initial population generation and the population size (Sivanandam and Deepa, 2008).
For each and every problem, the population size will depend on the complexity of the problem. It is often a random initialization of population is carried. In the case of a binary coded chromosome this means, that each bit is initialized to a random zero or one. But there may be instances where the initialization of population is carried out with some known good solutions.

Ideally, the first population should have a gene pool as large as possible in order to be able to explore the whole search space. All the different possible alleles of each should be present in the population. To achieve this, the initial population is, in most of the cases, chosen randomly. Nevertheless, sometimes a kind of heuristic can be used to seed the initial population. Thus, the mean fitness of the population is already high and it may help the genetic algorithm to find good solutions faster. But for doing this one should be sure that the gene pool is still large enough. Otherwise, if the population badly lacks diversity, the algorithm will just explore a small part of the search space and never find global optimal solutions.
The size of the population raises few problems too. The larger the population is, the easier it is to explore the search space. But it has established that the time required by a GA to converge is O (nlogn) function evaluations where n is the population size. We say that the population has converged when all the individuals are very much alike and further improvement may only be possibly by mutation. Goldberg has also shown that GA efficiency

to reach global optimum instead of local ones is largely determined by the size of the population. To sum up, a large population is quite useful. But it requires much more computational cost, memory and time. Practically, a population size of around 100 individuals is quite frequent, but anyway this size can be changed according to the time and the memory disposed on the machine compared to the quality of the result to be reached.

Population being combination of various chromosomes is represented as in figure 3.2. This population consists of four chromosomes.

Figure 3.2 Population of chromosomes

Population	Chromosome 1	1 1 1 0 0 0 1 0
	Chromosome 2	0 1 1 1 1 0 1 1
	Chromosome 3	1 0 1 0 1 0 1 0
	Chromosome 4	1 1 0 0 1 1 0 0

3.6.4 Search strategies

The search process consists of initializing the population and then breeding new individuals until the termination condition is met. There can be several goals for the search process, one of which is to find the global optima. This can never be assured with the types of models that GAs work with. There is always a possibility that the next iteration in the search would produce a better solution. In some cases, the search process could run for years and does not produce any better solution than it did in the first little iteration.

Another goal is faster convergence. When the objective function is expensive to run, faster convergence is desirable, however, the chance of converging on local and possibly quite substandard optima is increased.

Apart from these, yet another goal is to produce a range of diverse, but still good solutions. When the solution space contains several distinct optima, which are similar in fitness, it is useful to be able to select between them, since some combinations of factor values in the model may be more feasible than others. Also, some solutions may be more robust than others.

3.6.5 Encoding

Encoding is a process of representing individual genes. The process can be performed using bits, numbers, trees, arrays, lists or any other objects. The encoding depends mainly on solving the problem. For example, one can encode directly real or integer numbers.

3.6.6 Breeding

The breeding process is the core of the genetic algorithm. It is in this process, that the search process creates new and hopefully fitter individuals. The breeding cycle consists of three steps:

a. Selecting parents.

b. Crossing the parents to create new individuals (offspring or children).

c. Replacing old individuals in the population with the new ones.

3.6.6.1 Selection process

Selection is the process of choosing two parents from the population for crossing. After deciding on an encoding, the next step is to decide how to perform selection i.e., how to choose individuals in the population that will create offspring for the next generation and how many offspring each will create. The purpose of selection is to emphasize fitter individuals in the population in hopes that their offsprings have higher fitness. Chromosomes are selected

from the initial population to be parents for reproduction. The problem is how to select these chromosomes. According to Darwin's theory of evolution the best ones survive to create new offspring.

Selection is a method that randomly picks chromosomes out of the population according to their evaluation function. The higher the fitness function, the more chance an individual has to be selected. The selection pressure is defined as the degree to which the better individuals are favored. The higher the selection pressured, the more the better individuals are favored. This selection pressure drives the GA to improve the population fitness over the successive generations.

Genetic Algorithms should be able to identify optimal or nearly optimal solutions under a wise range of selection scheme pressure. However, if the selection pressure is too low, the convergence rate will be slow, and the GA will take unnecessarily longer time to find the optimal solution. If the selection pressure is too high, there is an increased change of the GA prematurely converging to an incorrect (sub-optimal) solution. In addition to providing selection pressure, selection schemes should also preserve population diversity, as this helps to avoid premature convergence.

Typically we can distinguish two types of selection scheme, proportionate selection and ordinal-based selection. Proportionate-based selection picks out individuals based upon their fitness values relative to the fitness of the other individuals in the population. Ordinal-based selection schemes selects individuals not upon their raw fitness, but upon their rank within the population. This requires that the selection pressure is independent of the fitness distribution of the population, and is solely based upon the relative ordering (ranking) of the population.

Selection has to be balanced with variation form crossover and mutation. Too strong selection means sub optimal highly fit individuals will take over the population, reducing the diversity needed for change and progress; too weak selection will result in too slow evolution. The various selection methods are discussed as follows:

3.6.6.1.1 Roulette selection

Roulette selection is one of the traditional GA selection techniques. The commonly used reproduction operator is the proportionate reproductive operator where a string is selected from the mating pool with a probability proportional to the fitness. The principle of roulette selection is a linear search through a roulette wheel with the slots in the wheel weighted in proportion to the individual's fitness values. A target value is set, which is a random proportion of the sum of the fit nesses in the population. The population is stepped through until the target value is reached. This is only a moderately strong selection technique, since fit individuals are not guaranteed to be selected for, but somewhat have a greater chance. A fit individual will contribute more to the target value, but if it does not exceed it, the next chromosome in line has a chance, and it may be weak. It is essential that the population not be sorted by fitness, since this would dramatically bias the selection.

3.6.6.1.2 Random Selection

This technique randomly selects a parent from the population. In terms of disruption of genetic codes, random selection is a little more disruptive, on average, than roulette wheel selection

3.6.6.1.3 Rank Selection

The Roulette wheel will have a problem when the fitness values differ very much.
If the best chromosome fitness is 90%, its circumference occupies 90% of Roulette wheel, and then other chromosomes have too few chances to be selected. Rank Selection ranks the

population and every chromosome receives fitness from the ranking. The worst has fitness 1 and the best has fitness N. It results in slow convergence but prevents too quick convergence. It also keeps up selection pressure when the fitness variance is low. It preserves diversity and hence leads to a successful search. In effect, potential parents are selected and a tournament is held to decide which of the individuals will be the parent. There are many ways this can be achieved and two suggestions are,

1. Select a pair of individuals at random. Generate a random number, *R*, between 0 and 1. If $R < r$ use the first individual as a parent. If the $R >= r$ then use the second individual as the parent. This is repeated to select the second parent. The value of *r* is a parameter to this method.

2. Select two individuals at random. The individual with the highest evaluation becomes the parent. Repeat to find a second parent.

3.6.6.1.4 Tournament Selection

Unlike, the Roulette wheel selection, the tournament selection strategy provides selective pressure by holding a tournament competition among N_i individuals.

The best individual from the tournament is the one with the highest fitness, which is the winner of N_i. Tournament competitions and the winner are then inserted into the mating pool. The tournament competition is repeated until the mating pool for generating new offspring is filled. The mating pool comprising of the tournament winner has higher average population fitness. The fitness difference provides the selection pressure, which drives GA to improve the fitness of the succeeding genes. This method is more efficient and leads to an optimal solution.

3.6.6.1.5 Boltzmann Selection

In Boltzmann selection a continuously varying temperature controls the rate of selection according to a preset schedule. The temperature starts out high, which means the selection pressure is low. The temperature is gradually lowered, which gradually increases the selection pressure, thereby allowing the GA to narrow in more closely to the best part of the search space while maintaining the appropriate degree of diversity.

3.6.6.2 Crossover process

After the required selection process the crossover operation is used to divide a pair of selected chromosomes into two or more parts. Parts of one of the pair are joined to parts of the other pair with the requirement that the length should be preserved.

The point between two alleles of a chromosome where it is cut is called crossover point. There can be more than one crossover point in a chromosome. The crossover point i is the space between the allele in the ith position and the one in $(i + 1)$th position. For two chromosomes the crossover points are the same and the crossover operation is the swapping of similar parts between the two chromosomes. The crossover operation may produce new chromosomes which are less fit. In that sense the crossover operation results in non-improving solution. The following are crossover operations that can be applied on chromosomes:

3.6.6.2.1 Single point crossover

The traditional genetic algorithm uses single point crossover, where the two mating chromosomes are cut once at corresponding points and the sections after the cuts exchanged. Here, a cross-site or crossover point is selected randomly along the length of the mated strings

and bits next to the cross-sites are exchanged. If appropriate site is chosen, better children can be obtained by combining good parents else it hampers string quality.

The figure 3.3 illustrates single point crossover and it can be observed that the bits next to the crossover points are exchanged to produce children. This crossover points can be chosen randomly.

Figure 3.3 single point crossover

Parent 1	10110 |010
Parent 2	10101|111
	|
Child 1	10110|111
Child 2	10101|010

To solve a traveling salesman problem, a simple crossover reproduction scheme does not work as it makes the chromosomes inconsistent. That is, some cities may be repeated while others are missing out. This drawback of the simple crossover mechanism is illustrated below;

Parent 1	1	2	3	4	|	5	6	7
Parent 2	3	7	6	1	|	5	2	4
Offspring 1	1	2	3	4	|	5	2	4
Offspring 2	3	7	6	1	|	5	6	7

From the illustration, cities 6 and 7 are missing in offspring1 whiles cities 2 and 4 are visited more than once. Offspring 2 too suffers from similar drawbacks. This drawback is avoided in partially matched crossover mechanism which is discussed in (iv).

3.6.6.2.2 Double point crossover

Apart from single point crossover, many different crossover algorithms have been devised, often involving more than one cut point. Adding more crossover points has the tendency to

reduce the performance of the genetic algorithm. The problem with adding additional crossover points is that building blocks are more likely to be disrupted. However, an advantage of having more crossover points is that the problem space may be searched more thoroughly.

In double point crossover, two crossover points are chosen and the contents between these points are exchanged between two mated parents.

In figure 3.4 the dotted lines indicate the crossover points. Thus the contents between these points are exchanged between the parents to produce new children for mating in the next generation.

Figure 3.4 Double point crossover

Parent 1	11011010
Parent 2	01101100

Child 1	11001110
Child 2	01111000

Originally, genetic algorithms were using single point crossover which cuts two chromosomes in one point and splices the two halves to create new ones. But with this single point crossover, the head and the tail of one chromosome cannot be passes together to the offspring. If both the head and the tail of a chromosome contain good genetic information, none of the offspring obtained directly with single point crossover will share the two good features. Using double point crossover avoids this drawback and then, is largely considered better than single point crossover. In genetic representation, genes that are close on a chromosome have more chance to be passed together to the offspring than those that are not. To avoid all the problem of gene positioning, a good crossover technique is to use a uniform crossover as recombination operator.

3.6.6.2.3 Multi-point crossover (N-Point crossover)

There are two ways in this crossover. One is even number of cross-sites and the other odd number of cross-sites. In the case of even number of cross-sites, cross-sites are selected randomly around a circle and information is exchanged. In the case of odd number of cross-sites, a different cross-point is always assumed at the string beginning.

3.6.6.2.4 Uniform crossover

In uniform crossover each gene in the offspring is created by copying the corresponding gene from one or the other parent chosen according to a random generated binary crossover mask of the same length as the chromosomes. Where there is a 1 in the crossover mask, the gene is copied from the first parent, and where there is a 0 in the mask the gene is copied from the second parent. A new crossover mask is randomly generated from each pair parents. Offsprings, therefore contain a mixture of genes from each parent. The number of effective crossing point is not fixed, but will average L/2, where L is the chromosome length.

In figure 3.5, new children are produced using uniform crossover approach. It can be noticed, that while producing child 1, when there is a 1 in the mask, the gene is copied from the parent 1 else from the parent 2. On producing child 2, when there is a 1 in the mask, the gene is copied from parent 2, when there is a 0 in the mask; the gene is copied from the parent 1.

Figure 3.5 uniform crossover

Parent 1	1 0 1 1 0 0 1 1
Parent 2	0 0 0 1 1 0 1 0
Mask	1 1 0 1 0 1 1 0
Child 1	1 0 0 1 1 0 1 0
Child 2	0 0 1 1 0 0 1 1

3.6.6.2.5 Partially matched crossover (PMX)

This aligns two chromosomes or strings and two crossover points are selected uniformly at random along the length of the chromosomes. The two crossover points give a matching selection, which is used to affect a cross through position-by-position exchange operations.

Consider two strings:

Parent A	4	8	7	|	3	6	5	|	1	10	9	2
Parent B	3	1	4	|	2	7	9	|	10	8	6	5

Two crossover points were selected at random, and PMX proceeds by position wise exchanges. In-between the crossover points the genes get exchanged. That is, the 3 and the 2, the 6 and the 7, the 5 and the 9 exchange places. This is by mapping parent B to parent A. now mapping parent A to parent, the 7 and the 6, the 9 and the 5, the 2 and the 3 exchange places. Thus after PMX, the offspring produces as follows:

Child A	4	8	6	|	2	7	9	|	1	10	5	3
Child B	2	1	4	|	3	6	5	|	10	8	7	9

Where each offspring contains ordering information which are partially determined by each of its parents.

Sometimes it may be possible that by crossover operation, a new population never gets generated. To overcome this limitation, we do mutation operation. Here we use insertion method, as a node along the optimal path may be eliminated through crossover.

3.6.6.3 Mutation process

After crossover, the strings are subjected to mutation. Mutation prevents the algorithm from been trapped in a local minimum. Mutation plays the role of recovering the lost genetic

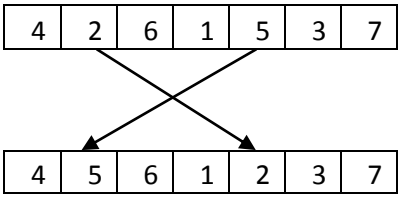
materials as well as for randomly disturbing genetic information. If crossover is supposed to exploit the current solution to find better ones, mutation is supposed to help for the exploration of the whole search space. Mutation introduces new genetic structures in the population by randomly modifying some of its building blocks. The building block being highly fit, low order, short defining length schemes, and encoding schemes. Mutation helps escape from local minima's trap and maintains diversity in the population.

There are many different forms of mutation for different kinds of representation. For binary representation, a simple mutation can consist in inverting the value of each gene with a small probability. The probability is usually taken about 1/L, where L is the length of the chromosome. Mutation of a bit involves flipping a bit, changing 0 to 1 and vice-versa. The following are some mutation carried on chromosomes:

i. Random swap mutation is when two loci (positions) are chosen at random and their values swapped.
ii. Move-and –insert gene mutation is when a locus is chosen at random and its value is inserted before or after the value at another randomly chosen locus.
iii. Move-and –insert sequence mutation is very similar to the gene move-and –insert but instead of a single locus a sequence loci is moved and inserted before or after the value at another randomly chosen locus.
iv. Uniform mutation probability sets a probability parameter and for all the loci an allele with greater or same probability as the parameter is mutated by reversing its allele

For the TSP problem, mutation refers to a randomized exchange of cities in the chromosomes. For instance, consider the example shown in figure 3.6. Here cities 2 and 5 are interchanged because of an inversion operation.

Figure 3.6 Mutation



3.6.6.4 Replacement

Replacement is the last stage of any breeding cycle. Two parents are drawn from a fixed size population, they breed two children, but not all four can return to the population, so two must be replaced. That is, once offsprings are produced, a method must determine which of the current members of the population, if any, should be replaced by new solution. The technique used to decide which individual stay in a population and which are replaced in on a par with the selection in influencing convergence. Basically, there are two kinds of methods for maintaining the population; generational updates and steady state updates.

In a steady state update, new individuals are inserted in the population as soon as they are created, as opposed to the generational update where an entire new generation is produced at each time step. The insertion of a new individual usually necessitates the replacement of another population member.

3.6.6.5 Search Termination (Convergence criteria)

The algorithm terminates when a conditions is satisfied. At that point the solution with best fitness among the current generation of the population is taken as the global solution or the algorithm may terminate if one or more of the following are satisfied:

i. a specified number of total iterations are completed;
ii. a specified number of iterations are completed within which the solution of best fitness has not change;

iii. Specified number of iterations are completed in which worst individual terminates the search when the least fit individuals in the population have fitness less than the convergence criteria. This guarantees the entire population to be of minimum standard.

iv. When the sum of fitness in the entire population is less than or equal to the convergence value in the population recorded.

v. Using a median fitness criteria. Here at least half of the individuals will be better than or equal to the convergence value, which should have a good range of solution to choose from.

3.7 Simple Genetic Algorithm (SGA)

An algorithm is a series of steps for solving a problem. A genetic algorithm is a problem solving method that uses genetics as its model of problem solving. It's a search technique to find approximate solutions to optimization and search problems.

Simple Genetic Algorithm (SGA) presented by Goldberg (1989) is an algorithm that captures most essential components of every genetic algorithm. The structure of genetic algorithm usually starts with guesses and attempts to improve the guesses by evolution. A GA typically has the following aspects:

i) a representation of a guess called a chromosome can be a binary sting or a more elaborate data structure,

ii) an initial pool of chromosomes can be randomly produced or manually created,

iii) a fitness function measures the suitability of a chromosome to meet a specified objective,

iv) a selection function decides which chromosomes will participate in the evolution stage of the genetic algorithm make up by the crossover and mutation operators, and

v) a crossover operator and a mutation operator. The crossover operator exchange genes from two chromosomes and creates two new chromosomes. The mutation operator changes a gene in a chromosome and creates one new chromosome.

The simple Genetic Algorithm may be summarized into the following steps:

Step 1: Code the individual of the search space

Step 2: Initialize the generation counter (g=1)

Step 3: Choose initial generation of population (solution)

Step 4: Evaluate the fitness of each individual in the population

Step 5: Select individuals of best fitness ranking by fitness proportionate probability

Step 6: Apply crossover operation on selected parents

Step 7: Apply mutation operation on offspring

Step 8: Evaluate fitness of offspring

Step 9: Obtain a new generation of population by combining elements of the offspring and the old generation by keeping the generation size unchanged

Step 10: Stop, if termination condition is satisfied

Step 11: Else $g = g+1$

The parameters that govern the GA search process are:

a. Population size: - It determines how many chromosomes and thereafter, how much genetic material is available for use during the search. If there is too little, the search has no chance to adequately cover the space. If there is too much, the GA wastes time evaluating chromosomes.
b. Crossover probability: - It specifies the probability of crossover occurring between two chromosomes.
c. Mutation probability: - It specifies the probability of doing bit-wise mutation.
d. Termination criteria: - It specifies when to terminate the genetic search.

The SGAs are useful and efficient when the search space is large, complex or poorly understood; when the domain knowledge is scarce or expert knowledge is difficult to encode to narrow the search space; when no mathematical analysis is available; and when the traditional search methods fail.

3.7.1 Work example application of GA to TSP

We consider a TSP with eight cities in figure 3.0 and its distance matrix in Table 3.0.

Initial population P= $\{P_x\}$, where P_x is an array index that defines the order in which the cities are traversed to make up a tour. Each chromosome must contain each and every city exactly once as in figure 3.6

Figure 3.6 Chromosomes representing the tour.

1	2	3	4	5	6	7	8

This chromosome represents the tour starting from city 1 to city 8 and back to city 1.

The tour is defined by the arc d (1, 2), d (2, 3), d (3, 4), d (4, 5), d (5, 6), d (6, 7), d (7, 8) and d (8, 1). Stop when the optimal solution is obtained.

Iteration 1: g=0

Step 1:

We generate some random individual solutions and pick two of these solutions. We then evaluate their fitness. The shorter a route the higher its fitness value. These random solutions are;

P_1= {1-3-8-7-6-5-4-2}, with f_1=59

P_2= {1-2-3-5-4-6-7-8}, with f_2=43

Step 3:

This random individual solution represents the parents on which we apply a partially matched crossover (PMX) operation.

P_1= {1 3 8 | 7 6 | 5 4 2}

P_2= {1 2 3 | 5 4 | 6 7 8}

Crossover is performed in the centre region to yield the following offspring:

P_1~ = 1 3 8 5 4 HH2

P_2~ = 1 2 3 7 6 HH8

The 'H' positions are holes in the offspring left by the deliberate removal of alleles which would otherwise be replicated in the crossing region. These holes are filled by cross-referencing with the parent of the alternate chromosome. This can best be explained with this step:

1. Take the sixth hole in P_1~ at index 6, the missing allele value at this position in P_1 is 5.
2. Search along P_2 (the alternate parent of P_1~) and match the sixth allele encountered with a value of 5. This occurs in P_2 at index 4.
3. Fill H [6] in P_1~ with the allele found at P_1 [4], a value of 7.

Applying this process to the remaining holes, we obtain the following PMX offspring:

P_1' = 13854762

P_2' = 12376458

Step 4:

Apply mutation on the two offsprings. Allele index 3 is selected for inversion. The value is simply exchanged with the allele at an additional randomly selected index, let's say index 6, as follows:

iP_1' = 13754862

iP_2' = 12476358

Hence, allele positions 3 and 6 have been exchanged.

Evaluate the objective function:

iP_1' = (1-3-7-5-4-8-6-2), with f_1= 74 km

iP_2' = (1-2-4-7-6-3-5-8), with f_2= 54 km

We choose offspring iP_2' as new individual since it has a shorter tour length.

Step 5:

The new individual replaces the old individual to obtain a new population. Since the end condition is not met we continue the next iteration and set the counter $g=g+1$

3.8 Omicron Genetic Algorithm (OGA)

Using SGA as a reference point, another version called Omicron Genetic Algorithm (OGA) is a genetic algorithm designed specifically for the TSP. The following are steps used in OGA;

3.8.1 Codification

Every population of individual P_x of P is a valid TSP tour and is determined by the arcs *(i, j)* that compose the tour. The OGA uses *n*-ary codification unlike binary codification used in

SGA. Considering a TSP with 6 cities *c1,c2,c3,c4,c5* and *c6*, the tour defined by the arcs *(c1,c5), (c5,c3), (c3,c4), (c4,c2), (c2,c6)* and *(c6,c1)* will be codified with a string containing the visited cities in order, that is {*c1,c5,c3,c4,c2,c6*}.

3.8.2 Reproduction

In the OGA, two parents *(F_1 and F_2)* are randomly selected from the population *P*, as does an SGA reproduction. The selection of a parent is done based on a probability proportional to the fitness of each individual P_x, fitness $(P_x) \alpha 1/l (P_x)$. In OGA both parents randomly selected for reproduction generate only one offspring unlike the SGA where two parents generate two offspring. Once an offspring is generated in OGA, it replaces the oldest element of *P* unlike in SGA *p* offspring are obtained first to completely replace the old generation. In OGA population exchange are made in a progressive way to obtain a totally new generation.

3.8.3 Crossover and Mutation

To obtain an offspring who represents valid tour, the crossover and mutation operators are done in a single operation called Crossover-Mutation in OGA unlike the SGA where crossover and mutation are done separately. To perform the Crossover-Mutation, arcs of the problem are put in the roulette, where every arc has a weight *w* or a probability to be chosen. Crossover-Mutation gives a weight *w* of 1 to each arc *(i, j)* belonging to set A, that is $w_{(i,j)} = 1 \quad \forall (i,j) \in A$, then a weight of $O/2$ is added to each arc(i,j) of F_1, that is $w_{(i,j)} = w_{(i,j)} + O/2 \quad \forall_{i,j} \in F_1$, where Omicron ($O$) is an input parameter of the OGA. Iteratively, arcs are randomly chosen using the roulette in other to generate a new offspring.

To generate an offspring S_1, an arc of a parent with a high probability is selected and new information may be added to allow for the creation of a valid tour to participate in the roulette with probability greater than 0, which is similar to mutation. The value $O/2$ is used because there are two parents and then, $w_{max} = O+1$ may be interpreted as the maximum weight an arc

can have in the roulette (when the arc belongs to both parents). When the arc does not belong to any parent, it obtains the minimum weight w_{min} in the roulette, that is $w_{min}=1$. Then, O determines the relative weight between crossover and mutation.

Formally, while visiting city i, the probability of choosing an arc (i, j) to generate the offspring S_1 is defined by equation *(ii)*,

$$P_{(i,j)}=\begin{cases}\frac{w_{i,j}}{\sum_{\forall h\in Ni} w_{i,j}}, & if\ j \in N_i \\ 0, & otherwise\end{cases} \qquad (ii)$$

The OGA can be summarized into the following steps:

Step 1: coding the individuals in the search space

Step 2: initializing a generation counter u =0

Step 3: random generation of individuals Px from the initial population.

Step 4: selection of two parents through a roulette for reproduction

Step 5: perform crossover and mutation operation at the same time on the parents to obtain an offspring.

Step 6: update the population by replacing the oldest individual of Px with the new generation of the offspring.

Step 7: stop, if the termination condition is met else increase the generation counter u=u+1

3.8.4 Work example of the application of OGA to TSP

Step 1: Codification

We consider a TSP with eight cities c1, c2, c3, c4, c5, c6, c7 and c8 in figure 3.0

Initial population P= {P_x}, where P_x is an array index that defines the order in which the cities are traversed to make up a tour. The tour is defined by the arcs (c1, c2), (c2, c3), (c3, c4), (c4,c5), (c5, c6), (c6, c7), (c7,c8), (c8,c1) . O =4 and p=5 are considered for this example.

Step 2: Reproduction

We assume an initial population is composed of 5 randomly selected individual with their respective fitness f_x. N_{ci} is the set of cities not yet visited. This initial population is presented as;

First: P_1 ={c1, c2, c3, c4, c5, c6, c7, c8}, with f_1=46

Second: P_2 = {c1, c3, c4, c6, c7, c8, c2, c5}, with f_2=61

Third: P_3 = {c3, c5, c1, c6, c2, c4, c8, c7}, with f_3=84

Forth: P_4 = {c2, c7, c8, c4, c3, c6, c1, c2}, with f_4=74

Fifth: P_5 = {c7, c3, c8, c4, c3, c2, c5, c1}, with f_5=79

Two parents are randomly selected through the roulette where the weights of solutions in the roulette are their fitness. We assume the solutions P_2 and P_3 as the parents selected.

F_1 = {c1, c3, c4, c6, c7, c8, c2, c5} =

{(c1,c3),(c3,c4),(c4,c6),(c6,c7),(c7,c8),(c8,c2),(c2,c5),(c5,c1)}

F_2 = {c3, c5, c1, c6, c2, c4, c8, c7}

={(c3,c5),(c5,c1),(c1,c6),(c6,c2),(c2,c4),(c4,c8),(c8,c7),(c7,c3)}

Step 3: Crossover and mutation

Iteration 1

We assume c7 as the random initial city.

Then, N_{c7} is composed by {c1, c2, c3, c4, c5, c6, c8}

The arcs {(c7, c1), (c7, c2),(c7, c4),(c7,c5)} have weights of 1 in the roulette because they did not belong to any parent.

The arc (c7, c8) has weight of 1+ O = 5 in the roulette because it belongs to both parents.

The arcs {(c7, c3), (c7, c6)} have weights of 1+ $O/2$ =3 in the roulette because they belongs to one parents.

We assume arc (c7, c6) as randomly chosen through the roulette.

Iteration 2

We pick c6 as the random initial city.

Then, N_{c6} is composed by {c1, c2, c3, c4, c5, c8}

The arcs {(c6,c3), (c6,c5),(c6,c8)} have weights of 1 in the roulette because they did not belong to any parent.

The arcs {(c6, c1), (c6,c2),(c6,c4)} have weights of 1+ $O/2$ = 3 in the roulette because it belongs to one parent.

We assume arc (c6, c3) as randomly chosen through the roulette.

Iteration 3

We pick c3 as the random initial city.

Then, N_{c3} is composed by {c1, c2, c4, c5, c8}

The arcs {(c3,c2), (c3,c8)} have weights of 1 in the roulette because they does not belong to any parent.

The arcs {(c3, c1), (c3,c4),(c3,c5)} have weights of 1+ $O/2$ = 3 in the roulette because they belong to one parent.

We assume arc (c3, c4) as randomly chosen through the roulette.

Iteration 4

We pick c4 as the random initial city.

Then, N_{c4} is composed by {c1, c2, c5, c8}

The arc {(c4,c1),(c4,c5)} have minimum weight of 1 in the roulette because it does not belong to any parent.

The arcs {(c4,c8),(c4, c2)} have weights of 1+ $O/2$ = 3 in the roulette because it belongs to one parent.

We assume arc (c4, c1) as randomly chosen through the roulette.

Iteration 5

We assume c1 as the random initial city.

Then, N_{c5} is composed by {c2, c5, c8}

The arc {(c1,c2),(c1,c8)} have weights of 1 in the roulette because it does not belong to any parent.

The arc (c1,c5) has weights of 1+ O = 5 in the roulette because it belongs to both parent.

We pick arc (c1, c5) as randomly chosen through the roulette.

Iteration 6

We pick c5 as the random initial city.

Then, N_{c5} is composed by {c2, c8}

The arc (c5, c8) has weight of 1 in the roulette because it does not belong to any parent.

The arc (c5, c2) has weight of 1+ $O/2$ = 3 in the roulette because it belongs to one parent.

We assume arc (c5, c2) as randomly chosen through the roulette.

Iteration 7

We pick c2 as the random initial city.

Then, N_{c2} is composed by {c8}

The arc (c2, c8) has weight of 1+O/2 in the roulette because it belongs to one parent.

We assume (c2, c8) as the final arc.

The new offspring is S_1

={c7,c6,c3,c4,c1,c5,c2,c8}={(c7,c6),(c6,c3),(c3,c4),(c4,c1),(c1,c5),(c5,c2),(c2,c8)}.

S_1has 5 arcs in F_1 {(c7,c6),(c3,c4),(c1,c5),(c5,c2),(c2,c8)} and no arc in F_2. Additionally, S_1 has these arcs {(c6, c3), (c4, c1)} which does not belong to any parent.

Step 4: Population update

The new offspring S_1 replaces the oldest solution P_3

P_1 ={c1, c2, c3, c4, c5, c6, c7, c8}, with f_1=56

P_2 = {c1, c3, c4, c6, c7, c8, c2, c5}, with f_2=61

P_3 = {c7, c6, c5, c4, c3, c2, c1, c8}, with f_3=61

P_4 = {c2, c7, c8, c4, c3, c6, c1, c2}, with f_4=74

P_5 = {c7, c3, c8, c4, c3, c2, c5, c1}, with f_5=79

We continue with the next iteration until the end condition is satisfied.

3.9 New Strategies for OGA

New strategies referred to crossover, population update and heuristic information are proposed for OGA. Considering that the most relevant aspect mentioned in OGA is the crossover of multiple parents, this new version is called Multi-Parent OGA (MOGA).

3.9.1 Crossover

We consider the generation of offspring through the crossover of multiple parents. This idea is not new and it was proposed before Mühlenbein and Voigt (1995). More specifically, this strategy proposes that the *p* individuals of **P** are parents without any roulette intervention. Obviously, this crossover of *p* parents eliminates competition among individuals during reproduction. Nevertheless, the new population update strategy proposed in the next section will solve this completion problem. Considering that there are *p* parents instead of 2, a weight of O/*p* is added to each arc *(i, j)* belonging to every F_x, i.e. $w_{(i,j)} = w_{(i,j)} + O/p \ \forall (i,j) \in F_x$. This way, when an arc belongs to the *p* parents, the weight of the arc will be $w_{max} = O + 1$. When an arc does not belong to any parent, the weight of the arc will be $w_{min} = 1$. This is done to maintain the weight limits (w_{max} and w_{min}).

3.9.2 Population Update

To reduce the possibilities that a bad individual enters the population, a competition strategy among offspring is considered. This new strategy replaces the most traditional parent competition strategy. This strategy consists on the generation of *t* offspring *{S*1, ..., *St}* in one iteration. Only the offspring with the best fitness ($S_{best} \in \{S_1 \ldots S_t\}$) is chosen to enter *P*. As in

the OGA population update strategy, S_{best} replaces the oldest individual of the population. Notice that the same effect is obtained (competition among individuals) with a different strategy.

3.9.3 Heuristic Information

Good TSP tours are composed with high probability by arcs with short length. Thus, it seems a good idea to give them better weights in the roulette. Then, considering the heuristic information $\eta_{(i,j)} = 1/ d(i, j)$, the probability of choosing an arc (i, j) to generate the offspring S_1 is now defined by equation *(iii)*.

$$P_{(i,j)} = \begin{cases} \frac{{w_{i,j}}^{\alpha} * {\eta_{i,j}}^{\beta}}{\sum_{\forall h \in Ni} {w_{i,j}}^{\alpha} * {\eta_{i,j}}^{\beta}}, & if\ j \in N_i \\ 0, & otherwise \end{cases} \qquad (iii)$$

Where the input parameters α and β are defined as the relative influence between the weight of the genetic information and the heuristic information η.

3.9.4 Work example of the application of MPOGA to TSP

Step 1: Codification

We consider a TSP with eight cities c1, c2, c3, c4, c5, c6, c7 and c8 in figure 3.0

Initial population P= $\{P_x\}$, where P_x is an array index that defines the order in which the cities are traversed to make up a tour. The tour is defined by the arcs (c1, c2), (c2, c3) , (c3, c4) , (c4, c5), (c5, c6), (c6, c7), (c7, c8), (c8, c1). O =4 and p=5 are considered for this example. We choose β =2, α =0.1 because these values are widely acclaimed to produces good solution.

Step 2: Reproduction

We assume an initial population is composed of 5 randomly selected solutions with their respective fitnesses f_x. N_{ci} is the set of cities not yet visited. This initial population is presented as;

First: P_1 = {c1, c2, c3, c4, c5, c6, c7, c8}, with f_1=56

Second: P_2 = {c1, c3, c4, c6, c7, c8, c2, c5}, with f_2=61

Third: P_3 = {c3, c5, c1, c6, c2, c4, c8, c7}, with f_3=84

Forth: P_4 = {c2, c7, c8, c4, c3, c6, c1, c2}, with f_4=74

Fifth: P_5 = {c7, c3, c8, c4, c3, c2, c5, c1}, with f_5=79

Consider there are *p* parents randomly selected as P_1, P_2 and P_3.

F_1 = {c1, c2, c3, c4, c5, c6, c7, c8} =

{(c1,c2),(c2,c3),(c3,c4),(c4,c5),(c5,c6),(c6,c7),(c7,c8),(c8,c1)}

F_2 = {c1, c3, c4, c6, c7, c8, c2, c5} =

{(c1,c3),(c3,c4),(c4,c6),(c6,c7),(c7,c8),(c8,c2),(c2,c5),(c5,c1)}

F_3 = {c3, c5, c1, c6, c2, c4, c8, c7}

={(c3,c5),(c5,c1),(c1,c6),(c6,c2),(c2,c4),(c4,c8),(c8,c7),(c7,c3)}

Step 3: Crossover and mutation

Iteration 1

We assume c7 as the random initial city.

Then, N_{c7} is composed by {c1, c2, c3, c4, c5, c6, c8}

The arcs {(c7, c3), (c7, c6), (c7, c8)} have weights $w_{max} = O+1=5$ because they belong to *p* parents.

The arcs {(c7, c1), (c7, c2), (c7, c4), (c7, c5)} have weights w_{min} =1 because it does not belongs to any *p* parents.

We assume arc (c7, c6) as randomly chosen through the roulette.

Iteration 2

We assume c6 as the random initial city.

Then, N_{c6} is composed by {c1, c2, c3, c4, c5, c8}

The arcs {(c6, c1), (c6, c2), (c6, c4), (c6,c5)}have weights $w_{max} = O+1=5$ because they belong to *p* parents.

The arc {(c6, c3), (c6, c8)} have weights w_{min} =1 because it does not belongs to any *p* parents.

We assume arc (c6, c2) as randomly chosen through the roulette.

Iteration 3

We assume c5 as the random initial city.

Then, N_{c5} is composed by {c1, c2, c3, c4, c8}

The arcs {(c2, c1), (c2, c3), (c2, c4), (c2, c5), (c2, c8)} have weights $w_{max} = O+1=5$ because they belong to p parents.

No arc belongs to any p parents.

We assume arc (c2, c4) as randomly chosen through the roulette.

Iteration 4

We assume c4 as the random initial city.

Then, N_{c4} is composed by {c1, c3, c5, c8}

The arcs {(c4, c3), (c4, c5), (c4, c8)} have weights $w_{max} = O+1=5$ because they belong to p parents.

The arc (c4, c1) has weight $w_{min} =1$ because it does not belongs to any p parents.

We assume arc (c4, c3) as randomly chosen through the roulette.

Iteration 5

We assume c3 as the random initial city.

Then, N_{c3} is composed by {c1, c5, c8}

The arcs {(c3, c1), (c3, c5)} have weights $w_{max} = O+1=5$ because they belong to p parents.

The arc (c3, c8) has weight $w_{min} =1$ because it does not belongs to any p parents.

We assume arc (c3, c5) as randomly chosen through the roulette.

Iteration 6

We assume c5 as the random initial city.

Then, N_{c5} is composed by {c1, c8}

The arc {(c5, c1)} has weight $w_{max} = O+1=5$ because they belong to p parents.

The arc {(c5, c8)} has weight $w_{min} =1$ because it does not belongs to any p parents.

We assume arc (c5, c1) as randomly chosen through the roulette.

Iteration 7

We assume c1 as the random initial city.

Then, N_{c1} is composed by {c8}

The arc {(c1, c8)} has weight $w_{max} = O+1=5$ because it belongs to p parent.

The arc (c1, c8) is chosen because it is the unique representation of the roulette.

The best offspring is S_1

={c7,c6,c2,c4,c3,c5,c1,c8}={(c7,c6),(c6,c2),(c2,c4),(c4,c3),(c3,c5),(c5,c1),(c1,c8)}.

S_1has 3 arcs in F_1 {(c7,c6),(c4,c3),(c1,c8)}, 3 arcs in F_2{(c6,c7),(c4,c3),(c5,c1)} and 4 arcs in F_3{(c6,c2),(c2,c4),(c3,c5),(c5,c1)}.

The new best offspring S_{best}

={c7,c6,c2,c4,c3,c5,c1,c8}={(c7,c6),(c6,c2),(c2,c4),(c4,c3),(c3,c5),(c5,c1),(c1,c8)}.

Step 4: Population update

The best offspring S_{best} is chosen to enter P

P_1 = {c1, c2, c3, c4, c5, c6, c7, c8}, with f_1=56

P_2 = {c1, c3, c4, c6, c7, c8, c2, c5}, with f_2=61

P_3 = {c3, c5, c1, c6, c2, c4, c8, c7}, with f_3=84

P_4 = {c2, c7, c8, c4, c3, c6, c1, c2}, with f_4 =74

P_5 = {c7, c3, c8, c4, c3, c2, c5, c1}, with f_5=79

P_6 = {c7, c6, c2, c4, c3, c5, c1, c8}, with f_5= 68

We continue with the next iteration until the end condition is satisfied.

CHAPTER 4

DATA COLLECTION, ANALYSIS AND RESULTS

The network for the traveling salesman consists of nineteen (19) administrative centres of the National Health Insurance Scheme (NHIS) among which the total distance is to be minimized. These centres will be represented as nodes with their respective names as shown in Table 4.0.

Table 4.0 Nodes and their respective administrative centres

Nodes	Name of Centre
1	Sunyani Municipal
2	Berekum Municipal
3	Dormaa District
4	Jaman North
5	Jaman South
6	Kintampo North
7	Kintampo South
8	Nkoranza District
9	Pru
10	Sene

Nodes	Name of Centre
11	Tain District
12	Tano North
13	Tano South
14	Techiman Municipal
15	Atebubu
16	Asutifi District
17	Asunafo North
18	Asunafo South
19	Wenchi District

Figure 4.1 shown below is the geographical positioning of administrative centres of NHIS in Ghana. The focus of our study is Brong Ahafo region of Ghana.

Figure 4.1 Map of administrative centres of NHIS in Ghana.

The Table 4.1 below displays the matrix of edge distances (in Km) of direct road link between the nineteen (19) administrative centres of NHIS in the Brong Ahafo region with sunyani as the starting node. The vertices $v(i,i) = 0$, indicates distance between a node and itself. Where there is infinity (inf) means no direct link between nodes. The matrix of edge distances of road links between nodes is displayed in Table 4.1. They were obtained from the Ghana Highways Authority in sunyani.

Table 4.1 Display of matrix of edge distances of road link between nodes.

Node	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0	34	Inf	Inf	inf	Inf	Inf	Inf	Inf	Inf	Inf	41	54	66	Inf	70	Inf	inf	65
2	34	0	46	Inf	40	Inf	Inf	Inf	Inf	Inf	108	Inf	Inf	Inf	Inf	inf	Inf	Inf	Inf
3	inf	46	0	Inf	50	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf
4	Inf	Inf	Inf	0	32	142	Inf	Inf	Inf	Inf	60	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf
5	Inf	40	50	32	0	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf
6	Inf	Inf	Inf	142	Inf	0	32	Inf	78	Inf	88	Inf	Inf	60	130	Inf	Inf	Inf	Inf
7	Inf	Inf	Inf	Inf	Inf	32	0	44	Inf	Inf	Inf	Inf	Inf	64	Inf	Inf	Inf	Inf	Inf
8	Inf	Inf	Inf	Inf	Inf	Inf	44	0	Inf	Inf	Inf	Inf	Inf	30	64	Inf	Inf	Inf	Inf
9	Inf	Inf	Inf	Inf	Inf	78	Inf	Inf	0	Inf	Inf	Inf	Inf	Inf	69	Inf	Inf	Inf	Inf
10	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	0	Inf	Inf	Inf	Inf	68	Inf	Inf	Inf	Inf
11	Inf	108	Inf	60	Inf	88	Inf	Inf	Inf	Inf	0	Inf	Inf	Inf	Inf	Inf	Inf	Inf	33
12	41	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	0	36	Inf	Inf	Inf	Inf	Inf	Inf
13	54	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	36	0	Inf	Inf	52	20	Inf	Inf
14	66	Inf	Inf	Inf	Inf	60	64	30	Inf	Inf	Inf	Inf	Inf	0	Inf	Inf	Inf	Inf	30
15	Inf	Inf	Inf	Inf	Inf	130	Inf	64	69	68	Inf	Inf	Inf	Inf	0	Inf	inf	Inf	Inf
16	70	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	52	Inf	inf	0	30	Inf	Inf
17	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	20	Inf	Inf	30	0	20	Inf
18	inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	20	0	inf
19	65	inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	inf	33	Inf	Inf	30	Inf	inf	Inf	Inf	0

Program code based on the Floyd-Warshall algorithm is used to compute all pair shortest possible path on the data in Table 4.1 to obtain a complete all pairs shortest path distance matrix which will be used for our analysis. The shortest path complete distance matrix is a complete undirected graph with vertices *v (i, j)*. The *v (i, i) = v (j, j)* = 0, indicates no distance between same node. The all pairs shortest path distance matrix is displayed in Table 4.2.

Table 4.2 Display of all pairs shortest path distance matrix $\{d_{i,j}\}$

Nodes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0	34	80	106	74	126	130	96	204	228	98	41	54	66	160	70	74	94	65
2	34	0	46	72	40	160	164	130	238	262	108	75	88	100	194	104	108	128	99
3	80	46	0	82	50	206	210	176	284	308	142	121	134	146	240	150	154	174	145
4	106	72	82	0	32	142	174	153	220	285	60	147	160	123	217	176	180	200	93
5	74	40	50	32	0	174	204	170	252	302	92	115	128	140	234	144	148	168	125
6	126	160	206	142	174	0	32	76	78	198	88	167	180	60	130	196	200	220	90
7	130	164	210	174	204	32	0	44	110	176	120	171	184	64	108	200	204	224	94
8	96	130	176	153	170	76	44	0	133	132	93	137	150	30	64	166	170	190	60
9	204	238	284	220	252	78	110	133	0	137	166	245	258	138	69	274	278	298	168
10	228	262	308	285	302	198	176	132	137	0	225	269	282	162	68	298	302	322	192
11	98	108	142	60	92	88	120	93	166	225	0	139	152	63	157	168	172	192	33
12	41	75	121	147	115	167	171	137	245	269	139	0	36	107	201	86	56	76	106
13	54	88	134	160	128	180	184	150	258	282	152	36	0	120	214	50	20	40	119
14	66	100	146	123	140	60	64	30	138	162	63	107	120	0	94	136	140	160	30
15	160	194	240	217	234	130	108	64	69	68	157	201	214	94	0	230	234	254	124
16	70	104	150	176	144	196	200	166	274	298	168	86	50	136	230	0	30	50	135
17	74	108	154	180	148	200	204	170	278	302	172	56	20	140	234	30	0	20	139
18	94	128	174	200	168	220	224	190	298	322	192	76	40	160	254	50	20	0	159
19	65	99	145	93	125	90	94	60	168	192	33	106	119	30	124	135	139	159	0

4.1 MODEL FORMULATION OF THE PROBLEM

The following assumptions and notations are used in developing the model:

Let:

i. The total number of nodes is n

ii. $d_{(i,j)}$ the distance between node i $(i=1,2,..,n)$ and node $j(j=1,2,\ldots,n)$ is obtained from Table 4.2 and n =19.

iii. for each link (i, j), $x_{(i,j)}=1$ if link (i, j) is part of the tour else $x_{(i,j)} = 0$

iv. The network is connected and therefore each city will be visited.

v. A is the set of arcs of the network.

Referring to model formulation in chapter 3 section 3.2. The tour length TL is defined as;

$$TL = \sum_{i,j}^{n} d_{(i,j)} x_{(i,j)}$$

Hence the problem for the TSP is;

$$\min \quad TL = \sum_{i,j}^{n} d_{(i,j)} x_{(i,j)} \qquad (1)$$

$$Subject\ to:$$

$$\sum_{i}^{n} x_{(i,j)} = 1 \qquad i = 1,\ldots,n \qquad (2)$$

$$\sum_{j}^{n} x_{(i,j)} = 1 \qquad j = 1,\ldots,n \qquad (3)$$

$$\sum_{i,j \in A} x_{(i,j)} \leq (n-1) \qquad (i,j) \in A, \qquad (4)$$

$$x_{(i,j)} \in \{0,1\} \qquad (i,j) \in A. \qquad (5)$$

The constraint (2) indicates that the salesman enter exactly one node. The constraint (3) ensures that each node depart to only one other node. The constraint (4) is the sub-tour elimination constraints which ensure that each tour has not more than *n*-1 arcs in the set of A. The constraint (5) is the integrality constraints that ensure the decision variable *x* is either 0 or 1. The $d_{(i,j)}$ elements in equation (1) is obtained from Table 4.2.

In this problem, the constraint two, three and five are considered. However, the condition of roads is not considered.

4.2 SOLUTION ALGORITHM (OMICRON GENETIC ALGORITHM)

Referring to steps in solving omicron genetic algorithm in chapter 3 sections 3.8.3. The solution algorithm is summarized into the following steps:

Step 1: coding the individuals in the search space

Step 2: initializing a generation counter *u* =0

Step 3: random generation of individuals P*x* from the initial population.

Step 4: selection of multi parents through a roulette for reproduction

Step 5: perform crossover and mutation operation at the same time on the parents to obtain

an offspring.

Step 6: update the population by replacing the oldest individual of P_x with the new generation of the offspring.

Step 7: stop, if the termination condition is met else increase the generation counter $u=u+1$

4.3 COMPUTATION PROCEDURE AND RESULTS

Matlab program code (Appendix A) was written to determine the optimal solution for the tour. This program was based on the omicron genetic algorithm.

The program was run on Dell inspiron 6000 with a processor speed of 2.0 GHz and 1.96 GB of RAM. Twenty one (21) number of runs and 100 iterations in each run. The input data is taken from Table 4.2.

4.3.1 THE COMPUTATIONAL PROCEDURES

Procedure 1: The centres were 19. A solution consists of permutation of numbers (n=1, 2, 3,…, 19). Nineteen (19) solutions formed a population.

Procedure 2: 21 runs each of 100 iterations were performed.

Procedure 3: generate nineteen random individuals as population.

Procedure 4: ten individuals are randomly selected from the population as parents through a roulette.

Procedure 5: perform crossover-mutation on two parents to generate an offspring.

Procedure 6: out of the ten individual selected as parents five offspring are generated from the first iteration and only the offsprings with better fitness are chosen to replace the weaker parent.

Procedure 7: continue from procedure 4

4.3.2 THE RESULTS

The Table 4.3 show the solution and fitness value obtained for each run.

Table 4.3 Display of solution and fitness value for each run.

No.:	Solution	Fitness value
1	1 13 3 15 16 11 14 19 9 10 2 6 18 12 8 7 17 4 5	1082
2	1 7 3 12 14 10 11 18 9 4 13 17 5 16 2 19 6 15 8	1234
3	1 15 2 5 18 11 7 13 17 14 4 6 10 8 19 12 9 16 3	1105
4	1 13 12 18 17 16 7 6 11 14 19 8 15 10 9 4 5 3 2	1120
5	1 12 18 17 13 16 3 10 7 6 9 15 8 19 14 11 4 5 2	1227
6	1 3 8 10 9 15 7 19 4 18 16 5 6 13 12 17 2 11 14	1116
7	1 15 18 4 19 2 12 6 17 13 14 11 9 8 3 7 10 5 16	1174
8	1 13 17 16 18 6 9 15 10 3 2 5 4 11 19 8 7 14 12	1364
9	1 19 11 2 3 5 4 7 6 9 10 15 8 14 12 13 17 18 16	1170
10	1 14 6 7 8 19 2 3 12 13 17 18 16 15 10 9 11 4 5	1191
11	1 13 3 15 16 11 14 19 9 10 2 6 18 12 8 7 17 4 5	1082
12	1 16 18 3 5 4 11 17 13 12 8 15 10 9 7 6 14 19 2	1263
13	1 7 4 6 9 16 3 15 5 2 10 12 8 11 17 14 13 19 18	1182
14	1 13 3 15 16 11 14 19 9 10 2 6 18 12 8 7 17 4 5	1082
15	1 13 3 15 16 11 14 19 9 10 2 6 18 12 8 7 17 4 5	1082
16	1 16 18 3 5 4 11 17 13 12 8 15 10 9 7 6 14 19 2	1263
17	1 13 3 15 16 11 14 19 9 10 2 6 18 12 8 7 17 4 5	1082
18	1 16 18 3 5 4 11 17 13 12 8 15 10 9 7 6 14 19 2	1263
19	1 7 4 6 9 16 3 15 5 2 10 12 8 11 17 14 13 19 18	1182
20	1 17 3 5 7 13 15 10 18 6 2 12 8 4 9 14 11 16 19	1047
21	1 14 8 10 9 15 7 6 19 11 4 5 2 3 16 17 18 13 12	1042

The results from Table 4.3 show that the twenty-first run has the minimum fitness value of 1042 km, which represents the order in which the nodes will be visited. The tour is represented as;

Sunyani Municipal (starting node) ⟶ Techiman Municipal⟶Nkoranza District⟶Sene ⟶ Pru⟶Atebubu ⟶ Kintampo South ⟶ Kintampo North ⟶ Wenchi District⟶ Tain District⟶Jaman North⟶ Jaman South ⟶ Berekum Municipal ⟶Dormaa District⟶ Asutifi District⟶ Asunafo North⟶Asunafo South ⟶Tano South⟶Tano North

Appendix B displays the steps and results in one iteration.

4.3.3 DISCUSSION

This work presented a study for finding optimal distance selection technique using omicron genetic algorithm. The results show a valid tour of optimal value 1042 km. Here the best tour

was obtained based on the minimum fitness value. The order in which the nodes will be visited is;

1 - 14 - 8 - 10 - 9 - 15 - 7 - 6 - 19 - 11- 4 - 5 - 2 - 3 - 16 - 17 - 18 - 13 - 12

This represents the tour;

Sunyani Municipal (starting node) ⟶ Techiman Municipal⟶Nkoranza District⟶Sene⟶ Pru⟶Atebubu⟶ Kintampo South⟶ Kintampo North⟶ Wenchi District⟶ Tain District⟶Jaman North⟶ Jaman South⟶ Berekum Municipal⟶ Dormaa District⟶ Asutifi District⟶ Asunafo North⟶Asunafo South ⟶Tano South⟶Tano North

CHAPTER 5

CONCLUSION AND RECOMMENDATION

5.1 CONCLUSION

This research work used the TSP model taking into account physical road distances in order to determine the optimal route for inspection tour of the administrative centres of NHIS in the Brong Ahafo region. The study applied omicron genetic algorithm for finding the optimum route. The results show a valid tour of optimal value of 1042 km. Here the best inspection tour was obtained based on the minimum fitness value. The preferred route is;

Sunyani Municipal (starting node) ⟶ Techiman Municipal⟶Nkoranza District⟶Sene⟶ Pru⟶Atebubu⟶ Kintampo South⟶ Kintampo North ⟶ Wenchi District⟶Tain District⟶Jaman North⟶ Jaman South⟶ Berekum Municipal⟶ Dormaa District⟶ Asutifi District⟶ Asunafo North⟶Asunafo South ⟶Tano South⟶Tano North

We conclude that the objective of the research was successfully achieved through the application of Omicron Genetic Algorithm.

5.2 RECOMMENDATION

Upon a study of application of Omicron Genetic Algorithm to Traveling Salesman Problem for inspection tour of the National Health Insurance Schemes, the following recommendation could be considered:

1. The NHIA office in the Brong Ahafo region may use this program code to optimize the inspection tour of the administrative centres of the NHIS.
2. Students may use this work for further research on omicron genetic algorithm.

REFERENCES

1. Ammar, E. E. and Youness, E. A. (2005). *Study on multiobjective transportation problem with fuzzy numbers*. Applied Mathematics and Computation. Vol. 166, pages 241-253.
2. Applegate, D., Bixby, R., Chvátal, V. and Cook, W. J. (2007). *The traveling salesman problem.* Princeton University Press: Princeton, NJ.
3. Beckers, R., Deneubourg, J. L. and Goss, S. (1992). Trails and U-turns in the selection of the shortest path by the ant Lasius niger. *Journal of Theoretical Biology*, Vol. 159, pages 397–415.
4. Bland, R. G. and Shallcross, D. F. (1989). *"Large Travelling Salesman Problems arising from Experimentsin X-ray Crystallography: A Preliminary Report on Computation".* Operations Research Letters. Vol 8, pages 125-128.
5. Miller, B. and Goldberg, D. E. (1995). "Genetic algorithm, Tournamanet selection and effect of noise, journal computer systems. Vol. 9, pages 193-212.
6. Caro, G. D. and Dorigo, M. (1998). "Extending AntNet for best-effort quality-of-service routing," Proceedings of the First Internation Workshop on Ant Colony Optimization (ANTS'98). Accessed at: (http://en.wikipedia.org/ Ant_colony_optimization.htm). Accessed on 27/11/2010.
7. Chen, W. N., ZHANG, J. and Chung, H. (2010). "Optimizing Discounted Cash Flows in Project Scheduling. An Ant Colony Optimization Approach", IEEE Transactions on Systems, Man, and Cybernetics. Part C: Applications and Reviews. Vol.40 No.5, pages 64-77.
8. Crowder, H. and Padberg, M. W. (1980). "Solving Large-Scale Symmetric Travelling Salesman Problems to Optimality". Management Science. Vol. 26, pages 495-509.
9. Dawkins, R. (1986). The Blind Watchmaker, Penguin, London.

10. Dantzig, G. B., Fulkerson, D. R. and Johnson, S. M. (1954). “Solution of a large-Scale Traveling-Salesman Problem”. Operation Research. Vol. 2, pages 393-410.

11. Dorigo, M. (1992). *Optimization, Learning and Natural Algorithms*, PhD thesis, Politecnico di Milano, Italy.

12. Garey, M. R. and Johnson D. S. (1979). *Computers and Intractability: A Guide to the Theory of NP-Completeness*, W. H. Freeman, San Francisco.

13. Gerard, Reinelt (1994). The Traveling Salesman: Computational Solution for TSP Applications. Springer-Verlag, Berlin.

14. Goldberg, D. E. (1989). *"Genetic Algorithms in Search, Optimization, and Machine Learning".* Addison-Wesley, New York.

15. Glover, F. (1986). “Future Paths for Integer Programming and Links to Artificial Intelligence”, *Computers and Operations Research*. Vol 13, pages 533-549.

16. Glover, F., Kelly, J. P. and Laguna, M. (1995). Genetic Algorithms and Tabu Search: Hybrids for Optimization. *Computers and Operations Research*. Vol. 22, No. 1, pages 111 – 134.

17. Grotschel, M. and Holland, O. (1991). “Solution of large-scale traveling salesman Problem”. Mathematical Programming. Vol. 51(2), pages 141-202.

18. Gutin, G., Yeo, A. and Zverovich, A. (2002). "Traveling salesman should not be greedy: domination analysis of greedy-type heuristics for the TSP", *Discrete Applied Mathematics.* Vol. 117 (1–3), pages 81–86.

19. Mühlenbein, H. and Voigt, H. (1995). Gene Pool Recombination in Genetic Algorithms. In Osman, H. I. and Kelly J. P., editors, *Proceedings of the Meta-heuristics Conference*, pages 53–62, Norwell, USA. Kluwer Academic Publishers.

20. Held, M. and Karp, R. M. (1971). “The Traveling Salesman Problem and Minimum Spanning Tress: Part II”. Mathematical Programming. Vol 1, pages 6-25.

21. Holland, J. (1975). “Adaptation In Natural and Artificial Systems,” University of Michigan Press, Ann Arbor, MI.

22. Hölldobler, B. and Wilson, E. O. (1990). *The ants* ,Springer-Verlag, Berlin.

23. Hillier, F.S. and Lieberman, G. J. (2005). Introduction to Operations Research. : McGraw-Hill. 8th Ed. New York, NY

24. Hu, X., Zhang, J. and Li, Y. (2008). Orthogonal methods based ant colony search for solving continuous optimization problems. *Journal of Computer Science and Technology*. Vol. 23(1), pages 2-18.

25. International Labour Organization (2005). Improving social protection for the poor: Health insurance in Ghana, The Ghana social trust pre-Piloted project final report. ISBN 92-2-117144-2.

26. Kutschera, U. (2003). *A Comparative Analysis of the Darwin-Wallace Papers and the Development of the Concept of Natural Selection*. Institut für Biologie, Universität Kassel, Germany.

27. Kirkpatrick, S., Gelett, C. D. and Vecchi, M. P. (1983). “*Optimization by Simulated Annealing"*. Science New Series Vol. 220, pages 671–680.

28. Lawler E. L., Lenstra J. K., Rinnooy Kan A. H. G. and Shmoys, D. B. (1986). *The Traveling Salesman.* John Wiley and sons. Chichester, UK,

29. Guntsch, M. and Middendorf, M. (2002). A Population Based Approach for ACO. In S. Cagnoni, J. Gottlieb, E. Hart, M. Middendorf, and G. Rinaldi, editors, *Applications of Evolutionary Computing, Proceedings of EvoWorkshops2002: EvoCOP, EvoIASP, EvoSTim*. Vol 2279, pages 71–80, Kinsale, Ireland, 3-4. Springer-Verlag, Berlin.

30. Guntsch, M. and Middendorf, M. (2002). Applying Population Based ACO to Dynamic Optimization Problems. In *Ant Algorithms, Proceedings of Third International Workshop ANTS 2002*, vol. 2463 of *LNCS*, pages 111–122.

31. Gómez, O. and Barán, B. (2004). Reasons of ACO's Success in TSP. In M. Dorigo, M. Birattari, C. Blum, L. M. Gambardella, F. Mondada, and T. Stützle, editors, *Proceedings of ANTS 2004 – Fourth International Workshop on Ant Colony Optimization and Swarm Intelligence*, vol. 3172 of *LNCS*, Brussels, Springer-Verlag, Berlin.

32. Gómez, O. and Barán, B. (2000). "Relationship between Genetic Algorithms and Ant Colony Optimization Algorithms". Available at: (http://www.cnc.una.py/invest/paper2/oga.pdf). Accessed on 27/11/2010.

33. Padberg, M. W and Rinaldi, G. (1987). "Optimization of a 532- city Symmetric Traveling Salesman Problem by Branch and Cut". *Operations Research Letters.* Vol. 6:17.

34. Papadimitriou, C. H. and Steglitz, K. (1997). *"Combinatorial Optimization: Algorithms and Complexity"*. Prentice Hall of India Private Limited, India.

35. Pham, D. T. and Karaboga, D. (2000). "Intelligent Optimisation Techniques – Genetic Algorithms, Tabu Search, Simulated Annealing and Neural Networks". London: Springer-Verlag, Berlin.

36. Ravikumar, C. P. (1992). *"Solving Large-scale Travelling Salesperson Problems on Parallel Machines"*.Microprocessors and Microsystems Vol. 16(3), pages 149-158.

37. Ray, S. S., Bandyopadhyay, S. and Pal, S. K. (2004). "New Operators of Genetic Algorithms for Traveling Salesman Problem", ICPR 2004, pages 129-170.

38. Rosenkrantz, D. J., Stearns, R. E. and Lewis, P. M. II (1977). "An Analysis of Several Heuristics for the Traveling Salesman Problem". *SIAM Journal on Computing* Vol. 6 (5), pages 563–581.

39. Sivanandam, S. N. and Deepa, S. N. (2008). "Introduction to Genetic Algorithms", Springer-Verlag Berlin Heidelberg.

40. Stützle, T. and Hoos, H. H. (2000). *MAX MIN Ant System*, Future Generation Computer Systems. Vol 16, pages 889-914.

41. Mahmoud, T. M. (2007). "A genetic and simulated annealing based algorithms for solving the flow assignment problem in computer Networks". World academy of science, engineering and technology. Vol. 38, pages 360-366.

42. Thomas, S. and Holger, H. H. (2000). *MAX-MIN* Ant System. *Future Generation Computer Systems*, Vol. 16(8), pages 889–914.

43. Zbigniew, M. (1994). Genetic Algorithms + Data Structures = Evolution Programs. Springer-Verlag, Berlin. 2nd edition.

Appendix A

MatLab Programme

```
function OmicronGeneticAlgorithm()
clear all;
clc;
try
%*******Load distance matrix from Table 4.2*********
dmat = load('output.txt');
catch
disp(sprintf('Error loading distance matrix from source:'));
end
pop_size=size(dmat,1);
n = pop_size;
numofparent=10;

% Verify Inputs
[nr,nc] = size(dmat);
if n ~= nr || n ~= nc
error('Invalid XY or DMAT inputs!')
end

% Initialize the Population
pop = zeros(n,n);
for k = 1:pop_size
pop(k,:) = randperm(n);
end

%initialize the combine population
combinepop=pop;

stop_criteria=100;
%*** Run the Omiron GA
number_of_iteration=1;
tic
fprintf('Initial Population\n')
disp(pop)
```

```
while number_of_iteration <=stop_criteria
fprintf('\nITERATION # = %d\n',number_of_iteration);
disp('**************************')
totalLenght = zeros(1,n);
dist_history_min = zeros(1,n);
dist_history_max = zeros(1,n);
dist_history_arc = zeros(1,n);
tempdist_inparent_history =zeros(1,n);
tempdist_not_inparent_history =zeros(1,n);
arc_distance =zeros(1,n);
totalTempdist_inparent = zeros(1,n);
totalTempdist_not_inparent = zeros(1,n);
dist_history_off_min=zeros(1,n);
parents=zeros(1,n);
offspring=zeros(1,n);
dist_promaxzero_p=zeros(1,n);
dist_promaxzero_np=zeros(1,n);
totalLenght = zeros(1,n);

sumpselect = 0;
for cv=1:n
    rantour = pop(cv,:);
    randtot=0;
    incr=1;
   for p=2:n
      rcvalue = dmat(rantour(incr),rantour(p));
      randtot = randtot + rcvalue;
      incr=incr+1;
   end
   totalLenght(cv)=randtot;
   %This calls a function to sum individual
   sumpselect = fcn_sum_individual(sumpselect,randtot);
   fprintf('\nPopulation #%d\t, Fitness value is =%d\n',cv,randtot)
end
spselect=0;
%Function for Roulette wheel selection, which returns results
[Excount,totalLenght,fitness]= fcn_RWS(sumpselect,n,totalLenght);
```

```
 % Find the Min Route in the Population
[min_dist,index1] = min(totalLenght);
dist_history_min(cv) = min_dist;

% Find the Max Route in the Population
[max_dist,index2] = max(totalLenght);
dist_history_max(cv) = max_dist;

fprintf('\nMinimum Fitness value = %d\n',min_dist)
fprintf('\nMaximum Fitness value = %d\n',max_dist)

cpcounter=0;
zeroparent=zeros(1,n);
fprintf('\nParents selected are:\n')
disp('-------------------------------------------------------')
for cparent=1:n
   if Excount(cparent) >= 1.0
      cpcounter=cpcounter+1;
      zeroparent(cparent) =cparent;
      if cpcounter==numofparent
         break
      end
   end
end
   %This is a function which returns parents selected
   [parents]=fcn_selectparent(zeroparent,parents,pop,numofparent);

   px=1;py=2; %for parent selection
for counter=1:numofparent,
   route_track = zeros(1,n);
   arc_in_parent=[];
   arc_not_in_parent=[];
   initNode = randperm(n);
   route = initNode; %NODES

   %begins. Generation of arcs
   counterarc=2;store_arcs1=[]; store_arcs2=[];
```

```
if  (py==numofparent) || (px<numofparent)
%This is a function which returns arc generated
[store_arcs1,store_arcs2]= fcn_looparc(counterarc,store_arcs1,store_arcs2,n,parents,px,py);
for iter=1:n,
if iter == 1
Node = initNode(iter); %pick a NODE
route(iter) = [0];
else
ind=find(route==Node);
route(ind)=[0];
end
%fprintf('\nNUMBER %d RANDOM INITIAL NODE = %d',iter,Node);
route_track(iter)=Node;
nonzeroindex=find(route~=0);
unvisitedNodes=route(nonzeroindex);

if (iter < n) & (~isempty(unvisitedNodes))

elseif (iter==n)  & (isempty(unvisitedNodes))
break;
end

%function to pick an arc generated
[arc_considered,arc_distance,arc_with_distance]=fcn_Generatearc(unvisitedNodes,route_track,iter,dm
at);

%Comparing and choosing of arcs
next=1;
distance_of_arc_in_parent=[];
tempdist_inparent=[];
distance_of_arc_not_in_parent=[];
tempmaxweigth=[];tempminweigth=[];
tempdist_not_inparent=[];
summaxweigth=0;summinweigth=0;
O =3;
for com1=1:length(unvisitedNodes)
for com2=1:n
```

```
  %comparing arc considered with first parent
if  (arc_considered(next,:)==store_arcs1(com2,:) |
fliplr(store_arcs1(com2,:))==arc_considered(next,:)) &  arc_considered(next,:)==store_arcs2(com2,:) |
arc_considered(next,:)==fliplr(store_arcs2(com2,:))

  [weight]= fcn_CMArc_twoparent(O);
end
if  arc_considered(next,:)==store_arcs1(com2,:) | fliplr(store_arcs1(com2,:))==arc_considered(next,:)

  %function to select arc in first parent
[heu_info,tempdist_inparent,distance_of_arc_in_parent,arc_in_parent]=fcn_select_arcinfirstparent(ne
xt,arc_considered,arc_in_parent,arc_with_distance,arc_distance,tempdist_inparent,distance_of_arc_in
_parent);
  [summaxweigth,maxweigth] = fcn_assume_max_arc(heu_info,summaxweigth);
  tempmaxweigth=[tempmaxweigth;maxweigth];
  [weight]=fcn_CMArc_oneparent(O);
else
  %function to select arc not found in first parent

[heu_info,tempdist_not_inparent,distance_of_arc_not_in_parent,arc_not_in_parent]=fcn_select_arcno
tinfirstparent(next,arc_considered,arc_not_in_parent,arc_with_distance,arc_distance,tempdist_not_inp
arent,distance_of_arc_not_in_parent);
  %Function for arc with Min weigth
  [summinweigth,minweigth] = fcn_assume_min_arc(heu_info,summinweigth);
  tempminweigth=[tempminweigth;minweigth];
  weigth=1;
  [weigth]=fcn_CMArc_noparent(weigth);
end
%comparing arc considered with next parent
if  arc_considered(next,:)==store_arcs2(com2,:) | arc_considered(next,:)==fliplr(store_arcs2(com2,:))
  %Function to select arc in next parent

[heu_info,tempdist_inparent,distance_of_arc_in_parent,arc_in_parent]=fcn_select_arcinfirstparent(ne
xt,arc_considered,arc_in_parent,arc_with_distance,arc_distance,tempdist_inparent,distance_of_arc_in
_parent);
  %Function for arc with Max weigth
  [summaxweigth,maxweigth] = fcn_assume_max_arc(heu_info,summaxweigth);
```

```
  tempmaxweigth=[tempmaxweigth;maxweigth];
  [weight]=fcn_CMArc_oneparent(O);
else
  %Function to select arc not found in next parent

[heu_info,tempdist_not_inparent,distance_of_arc_not_in_parent,arc_not_in_parent]=fcn_select_arcno
tinfirstparent(next,arc_considered,arc_not_in_parent,arc_with_distance,arc_distance,tempdist_not_inp
arent,distance_of_arc_not_in_parent);
  %Function for arc with Min weigth
  [summinweigth,minweigth] = fcn_assume_min_arc(heu_info,summinweigth);
  tempminweigth=[tempminweigth;minweigth];
  weigth=1;
  [weight]=fcn_CMArc_noparent(weigth);
end
  totalTempdist_inparent = tempdist_inparent;
  totalTempdist_not_inparent = tempdist_not_inparent;
end
   next=next+1;
end
%prob_of_choosing_arc
prob_of_choosing_arc_p_parent = tempmaxweigth/summaxweigth;
prob_of_choosing_arc_n_parent = tempminweigth/summinweigth;

% Finds the Min distance of p parents
[tempdist_inparent_min_dist ,tempdist_inparent_index] = min(totalTempdist_inparent);
tempdist_inparent_history = tempdist_inparent_min_dist;

% Find the Min distance of arc not in p parents
[tempdist_not_inparent_min_dist ,tempdist_not_inparent_index] = min(totalTempdist_not_inparent);
tempdist_not_inparent_history = tempdist_inparent_min_dist;

% Find the arc with higher probability in p parent
[maxprob_inp,pidx] = max(prob_of_choosing_arc_p_parent);
dist_promaxzero_p = maxprob_inp;

% Find the arc with higher probability not in p parent
[maxprob_np,pnidx] = max(prob_of_choosing_arc_n_parent);
```

```
dist_promaxzero_np = maxprob_np;

% Display arcs
if ~isempty(tempdist_inparent)
%SET ZEROS IN THE NEXT NODE
next_Node=zeros(1);
%PICKS THE NEXT NODE
Node=fcn_selectnodeinparent(tempdist_inparent_index,arc_in_parent,pidx);
elseif ~isempty(tempdist_not_inparent) & (isempty(tempdist_inparent))
%SET ZEROS IN THE NEXT NODE
next_Node=zeros(1);
%PICKS THE NEXT NODE
Node=fcn_selectnodenotinparent(tempdist_not_inparent_index,arc_not_in_parent,pnidx);
end
arc_in_parent=[]; %for arc picking
arc_not_in_parent=[];
end

%this keeps the offspring
offspring(counter,:)= route_track;

%Function to calculate distance for offspring
offspringtotalLenght=zeros(1,numofparent);
[offspringtotalLenght,tcv]=fcn_minDistforOffspring(offspringtotalLenght,n,dmat,offspring,counter);
%Finds index of offspring which are non zeros
offspringLenghtindex=find(offspringtotalLenght~=0);
offspringdistances = offspringtotalLenght(offspringLenghtindex);
[min_offspringdistances,offindx1] = min(offspringdistances);
dist_history_off_min(tcv) = min_offspringdistances;

%this append the offsprings to the initial population
tempcomindx=n+offspringLenghtindex;
combinepop(tempcomindx,:)=offspring(offspringLenghtindex,:);
%This appends the total length to the initial population
totalLenght(tempcomindx)=offspringdistances;
combinetotalLenght=totalLenght;
if py==numofparent
```

```
    [comvalue,comindx]=sort(combinetotalLenght);
    fprintf('\nBest solution in population are: \n')
    disp(offspring);
    fprintf('fitnesss value are: \n')
    disp(offspringdistances)
    disp('Combine population are:')
    disp(combinepop(comindx,:));
    disp('fitness value are:')
    disp(comvalue')
    pop=combinepop(comindx,:);  %for the next initial population
end

%THIS PART GENERATES THE subsequent ARCS FOR THE PARENTS
px = px+2;
py = py+2;
end
end
  number_of_iteration = number_of_iteration + 1;
   t = toc;
end
disp(t)
end

function [weigth]=fcn_CMArc_noparent(weigth)
%Function for arc with max weight
weight=1;
end

function [weight]=fcn_CMArc_oneparent(O)
%Function for arc with max weight
weight=1 + O/2;
end

function [weight]=fcn_CMArc_twoparent(O)
%Function for arc with max weight
weight=1 + 2*(O/2);
end
```

```
function [summaxweigth,weigth]=fcn_assume_max_arc(heu_info,summaxweigth)
beta=2.0; theta=0.3;
O=3;    %Omicron(O) parameter
w_max= O +1;
weigth =(w_max^theta * heu_info^beta);
summaxweigth = summaxweigth + weigth;
end

function [summinweigth,minweigth] = fcn_assume_min_arc(heu_info,summinweigth)
beta=2.0; theta=0.3;
w_min= 1;
summinweigth=0;
minweigth =(w_min^theta * heu_info^beta);
summinweigth= summinweigth + minweigth;
end

function [store_arcs1,store_arcs2]= fcn_looparc(counterarc,store_arcs1,store_arcs2,n,parents,px,py)
%This is a function which returns arc generated
for looparc=1:n
if looparc~=n
genarc1(looparc,:)=parents(px,[looparc counterarc]);
genarc2(looparc,:)=parents(py,[looparc counterarc]);
else
genarc1(looparc,:)=parents(px,[n 1]);
genarc2(looparc,:)=parents(py,[n 1]);
end
counterarc = counterarc + 1;
store_arcs1 = [store_arcs1; genarc1(looparc,:)];
store_arcs2 = [store_arcs2; genarc2(looparc,:)];
end
end

function
[offspringtotalLenght,tcv]=fcn_minDistforOffspring(offspringtotalLenght,n,dmat,offspring,counter)
%Function to calculate distance for all offspring generated
for tcv=1:counter
```

```
 temprantour = offspring(tcv,:);
 temprandtot=0;
 tincr=1;
for tp=2:n
temprcvalue = dmat(temprantour(tincr),temprantour(tp));
temprandtot = temprandtot + temprcvalue;
tincr=tincr+1;
end
offspringtotalLenght(tcv)=temprandtot;
end
end
```



```
function sumparent =fcn_sum_individual(sumparent,randtot)
%This sums the parent
sumparent = sumparent + randtot;
end
```

```
function   [Excount,totalLenght,fitness]= fcn_RWS(sumpselect,n,totalLenght)
%The roulette wheel selection function
spselect=0;
for sm=1:n
fitness(sm)=totalLenght(sm)/sumpselect;
%This calls a function sum individual
spselect = fcn_sum_individual(spselect,fitness(sm));
end
avgpselect=spselect/n;
for cavg=1:n
Excount(cavg)=fitness(cavg)/avgpselect;
end
end
```

```
function [parents]=fcn_selectparent(zeroparent,parents,pop,numofparent)
%This is a function which returns parents selected
%Finds non zero index
nonzeroparentindex=find(zeroparent~=0);
lenparentindex=length(nonzeroparentindex);
%This selects the number of parents
```

```
for selectx=1:numofparent
parents(selectx,:)= pop(selectx,:);
end
for selecty=1:numofparent
fprintf('Parent %d:',selecty);
disp(parents(selecty,:))
end
end
```

```
function [Node]=fcn_selectnodeinparent(tempdist_inparent_index,arc_in_parent,pidx)
%function to select node in p parent
if ~isempty(tempdist_inparent_index)
next_Node =arc_in_parent(pidx,2);
else
next_Node =arc_in_parent(pidx);
end
Node= next_Node;
end
```

```
function Node=fcn_selectnodenotinparent(tempdist_not_inparent_index,arc_not_in_parent,pnidx)
%function to select node not in p parent
if ~isempty(tempdist_not_inparent_index)
next_Node =arc_not_in_parent(pnidx,2);
else
next_Node =arc_not_in_parent(pnidx);
end
Node= next_Node;
end
```

```
function
[arc_considered,arc_distance,arc_with_distance]=fcn_Generatearc(unvisitedNodes,route_track,iter,dm
at)
%function to pick arc generated
arc_considered=[];
dist_arc_considered=[];
for y=1:length(unvisitedNodes)
  arc_considered =[arc_considered; route_track(iter) unvisitedNodes(y)];
```

```
if arc_considered ~=arc_considered,
  arc_considered=[arc_considered];
end
  dist_arc_considered=[dist_arc_considered;dmat(route_track(iter), unvisitedNodes(y))];
  arc_distance = dist_arc_considered;
end
[arc_min_dist,arcdist_index] = min(arc_distance);
dist_history_arc(y) = arc_min_dist;
arc_with_distance=[arc_considered, arc_distance];
end
```



```
function
[heu_info,tempdist_inparent,distance_of_arc_in_parent,arc_in_parent]=fcn_select_arcinfirstparent(ne
xt,arc_considered,arc_in_parent,arc_with_distance,arc_distance,tempdist_inparent,distance_of_arc_in
_parent)
%function to select arc in first parent
arc_in_parent =[arc_in_parent; arc_considered(next,:)];
distance_of_arc_in_parent=[distance_of_arc_in_parent; arc_with_distance(next,:)];
tempdist_inparent = [tempdist_inparent; arc_distance(next,:)];
heu_info= (1 /arc_distance(next,:));
end
```

```
function
[heu_info,tempdist_not_inparent,distance_of_arc_not_in_parent,arc_not_in_parent]=fcn_select_arcno
tinfirstparent(next,arc_considered,arc_not_in_parent,arc_with_distance,arc_distance,tempdist_not_inp
arent,distance_of_arc_not_in_parent);
%function to select arc not in first parent
arc_not_in_parent =[arc_not_in_parent; arc_considered(next,:)];
distance_of_arc_not_in_parent=[distance_of_arc_not_in_parent; arc_with_distance(next,:)];
tempdist_not_inparent = [tempdist_not_inparent; arc_distance(next,:)];
heu_info= (1 /arc_distance(next,:));
end
```

Appendix B

Computational Results obtained from MatLab program

```
ITERATION # = 1

Initial Population
------------------

Intpop1:[6  3  16 11   7  17  14   8   5  19  15   1   2   4  18  13   9  10  12],fitness=2607
Intpop2:[13  3 15 16 11  14  19   9  10   2   6   18  12  8   7   17   4   5   1],fitness=2559
Intpop3:[2  17  16  7  13   4  3   9   8  18  10   15  14  11  12  5   6   1  19],fitness=2537
Intpop4:[11  12  3  17  15  5  13  1  19   6  10   2   7   4   16  14  8  18   9],fitness=2847
Intpop5:[16  15  1  2  10  5  13  4  17   8  14   7   3   12  11  18  6   9   19],fitness=2848
Intpop6:[4   17  1  6  10  18 12  8   5  16   3   9   2  11   13  14  15  7   19],fitness=2775
Intpop7:[9   5  13   7  1   19 15  14  17  6  3  10  16  11   2   12  18  8   4],fitness=2899
Intpop8:[19  13  15  3  7  2  16  14  17   1  10  12  18  11   6   5   9   8   4],fitness=2966
Intpop9:[18  13  8  14  19  11  5  7  10  12   4   3  17   9   6   1   15  2  16],fitness=2347
Intpop10:[3  4  19   5  15  13  11  1  16   9  10  17   8  6  14   7   12  18  2],fitness=2526
Intpop11:[6  15  12   4  5  3  7   8  14  18  19  11   2  10  13   9   17  1  16],fitness=2528
Intpop12:[19  9  15  7   2  8  10  5  3   12  14  11  18   4   1   6   16  13 17],fitness=2304
Intpop13:[16  13  8   7  1  4  14  9  10   2  11  19  12   3   5   6   18  15 17],fitness=2440
Intpop14:[14  18  7  2  19  12  11  3  8   6   5   1   9  10  17  15   16  4  13],fitness=2977
Intpop15:[15  5  3  14  12  1  18  7  17   6  2  13   9   4  16   8   11  10  19],fitness=2878
Intpop16:[9  18 16  19  11  6  7  15  10  14   5  1   2  17  13   4   3   8   12],fitness=1905
Intpop17:[15  2  16   6  17  18  13  12  8  1  10  7   5  11   4   3  14  19  9],fitness=2209
Intpop18:[10  2  13  12  15  8  17  14  3  5  9  16  4   7   6   1   19  18  11],fitness=2607
Intpop19:[19  1  16  18  15  3  9  7  4  12  5  11   14  13  10  2   6   8   17],fitness=2734


Minimum Fitness value = 1905

Maximum Fitness value = 2977

Parents selected are:
---------------------------------------------------------
Parent 1: [6   3   16   11  7   17  14   8   5   19  15   1   2   4  8  13   9  10 12]

Parent 2: [13  3   15   16  11  14  19   9   10   2  6   18  12   8  7  17   4  5   1]

Parent 3: [2   17  16   7   13  4   3    9   8   18  10  15  14  11  12  5   6  1  19]

Parent 4: [11  12  3    17  15  5   13   1   19   6  10   2   7   4  16  14  8  18  9]

Parent 5: [16  15  1    2   10  5   13   4   17   8  14   7   3  12  11  18  6  9  19]

Parent 6: [4   17  1    6   10  18  12   8   5   16   3   9   2  11  13  14  15  7 19]

Parent 7: [9   5   13   7   1   19  15  14   17   6   3  10  16  11   2  12  18  8  4]

Parent 8: [19  13  15   3   7   2   16  14   17   1  10  12  18  11   6   5   9  8  4]

Parent 9: [18  13  8   14   19  11   5   7  10  12   4   3  17   9   6  1  15   2  16]

Parent 10:[3   4   19   5   15  13  11   1  16   9  10  17   8   6  14  7  12  18   2]


Best solutions are:
--------------------
B1: [15  19  14   8  7   11  16   3   13  18  12   6   2   1   5   4  17   9  10],fitness=1978
B2: [16  17   2  19  1   13   5  12   3   4    7   6  10  15  14   8   9  11  18],fitness=1889
B3: [ 9   6   1   2  11  12  18  10   5   13  14   8  17   4  19   7  15  16   3],fitness=2488
B4: [ 5  13  19   1  17  14  15   3   6   11   2  12  18   8   9   4   7  10  16],fitness=2604
B5: [15   1  16  18  13   8  14  19   11  5    7  12   4   3   2  17   9   6  10],fitness=1967
```

```
Combine population is:
------------------------
Cpop1:[16  17   2  19   1  13  5   12   3   4  7   6  10  15  14   8   9  11  18],fitness=1889
Cpop2:[9   18  16  19  11   6  7   15  10  14  5   1   2  17  13   4   3   8  12],fitness=1905
Cpop3:[15   1  16  18  13   8  14  19  11   5  7   12  4   3   2  17   9   6  10],fitness=1967
Cpop4:[15  19  14   8   7  11  16   3  13  18  12  6   2   1   5   4  17   9  10],fitness=1978
Cpop5:[15   2  16   6  17  18  13  12   8   1  10  7   5  11   4   3  14  19   9],fitness=2209
Cpop6:[19   9  15   7   2   8  10   5   3  12  14  11  18  4   1   6  16  13  17],fitness=2304
Cpop7:[18  13   8  14  19  11   5   7  10  12   4  3   17  9   6   1  15   2  16],fitness=2347
Cpop8:[16  13   8   7   1   4  14   9  10   2  11  19  12  3   5   6  18  15  17],fitness=2440
Cpop9:[ 9   6   1   2  11  12  18  10   5  13  14   8  17  4  19   7  15  16   3],fitness=2488
Cpop10:[ 3  4  19   5  15  13  11   1  16   9  10  17   8  6  14   7  12  18   2],fitness=2526
Cpop11:[ 6  15  12   4   5   3   7   8  14  18  19  11   2 10  13   9  17  1  16],fitness=2528
Cpop12:[ 2  17  16   7  13   4   3   9   8  18  10  15  14 11  12   5   6  1  19],fitness=2537
Cpop13:[13   3  15  16  11  14  19   9  10   2   6  18  12  8   7  17   4  5   1],fitness=2559
Cpop14:[5   13  19  1   17  14  15   3   6  11   2  12  18  8   9   4   7  10 16],fitness=2604
Cpop15:[6    3  16  11   7  17  14   8   5  19  15   1   2  4  18  13   9  10 12],fitness=2607
Cpop16:[10   2  13  12  15   8  17  14   3   5   9  16   4  7   6   1  19  18 11],fitness=2607
Cpop17:[19   1  16  18  15   3   9   7   4  12   5  11  14  13  10  2   6  8  17],fitness=2734
Cpop18:[ 4  17   1   6  10  18  12   8   5  16   3   9   2  11  13  14 15  7  19],fitness=2775
Cpop19:[11  12   3  17  15   5  13   1  19   6  10   2   7   4  16  14  8  18  9],fitness=2847
Cpop20:[16  15   1   2  10   5  13   4  17   8  14   7   3  12  11  18  6  9  19],fitness=2848
Cpop21:[15   5   3  14  12   1  18   7  17   6   2  13   9   4  16   8 11  10 19],fitness=2878
Cpop22:[ 9   5  13   7   1  19  15  14  17   6   3  10  16  11   2  12 18  8   4],fitness=2899
Cpop23:[19  13  15   3   7   2  16  14  17   1  10  12  18  11   6   5  9  8   4],fitness=2966
Cpop24:[14  18   7   2  19  12  11   3   8   6   5   1   9  10  17  15 16  4  13],fitness=2977


ITERATION # = 2
**************************

Population #1, Fitness value is =1889

Population #2, Fitness value is =1905

Population #3, Fitness value is =1967

Population #4, Fitness value is =1978

Population #5, Fitness value is =2209

Population #6, Fitness value is =2304

Population #7, Fitness value is =2347

Population #8, Fitness value is =2440

Population #9, Fitness value is =2488

Population #10      , Fitness value is =2526

Population #11      , Fitness value is =2528

Population #12      , Fitness value is =2537

Population #13      , Fitness value is =2559

Population #14      , Fitness value is =2604

Population #15      , Fitness value is =2607
```

```
Population #16      , Fitness value is =2607
Population #17      , Fitness value is =2734
Population #18      , Fitness value is =2775
Population #19      , Fitness value is =2847
Minimum Fitness value = 1889
Maximum Fitness value = 2847
```